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                                                                             CTCGCTGAACTTCGTCGAGCTGGAACAGAAGGTCGAGGGCCTGCTGGACAGCTACACCGA 1460
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Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MYCHION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBYCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
DETCE APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR TILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7413
LENGTH: 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.6%; Score 164.2; DB 4; Length 1083; Best Local Similarity 50.9%; Pred. No. 5.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1461 CCTGCTCAACCCGGACTTCGCCCGTCTCGCCGAAGTGATCGGCTTCCACGGACGCAAGGT 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1641 CCAGGTC 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1958 ACAGGTC 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1581 GCTGCTGGACGTGCATACCAACCCTGCGGAGCTGGTGATGCCGCCGAAGATCGAGTTCGG 1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1521 GACGCGCTCCGAGGAGCTCGAGACGGCGGTGCAGGAGTTCCTCGCCCAGCCCGGTCCGGC 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1838 CACCGATCCGAAGAAGTTCGCGAGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGT 1897
                  761 GTCCACCATGGCGGGTAAAGGTGTGTGGTGGTAGTGATTCCTGGTGATATCGCTAAGGA 820
                                                                                                                                            701 TTACTGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCA 760
                                                                                                                                                                                                                                      641 GATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGG
                                                                                                                                                                                                                                                                                        581 TGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCA 640
                                                                                                                                                                                                                                                                                                                                                                                                                                      521 GCTGGCAGTATGTGCTGCTTCTTGTGGTCCTGGAAACACACCTGATTCAGGGTCTTTA 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 CGTTCGAMATGAGGAAGCGGCGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 CGGCGACACCCTCAACCATGTCACCGACGCCATCCATCGCAGCCAGATCCAGTGGGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 GGGTGACAGCCTTAATCCGATCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 CGCAGAACAATTAATTGACACTTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 CGCCGAGATCGTCGTGGAAACCCTGGAAGCCGCCGGCGTCCGCCATTGCTATGGCATCGT 101
GTTCTGCGAGCAGGTGCACAGCCCGGAACAGGCGCGCGGGTGGTGGCCCTGGCCTGCCA
                                                                                                                                                                                             ACTGGGCATGGAGTTTCCCCCAGGAGGTCGACTTCAAGGCGGTCTACGCCAGCTGCTCGGT 401
                                                                                                                                                                                                                                                                                                                                                                                          CCTGACCGCCTGCGGCTCCTGCGGACCGGGCAGCCTGCACTTCATCAACGGCGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTGCGCCACGAAGAAGCGGCGGCGTTCGCCGCGGGCGCCGAGTCCTACATCAGCGGACG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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517
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO A TITLE OF INVENTION: AERGGINOSA FOR DIAGNOSTI FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-252-991A-7281/c
                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-7281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SEQ ID NO 7281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7281, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1113
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                1000
                                                                                                                                                                                                                                       1060
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                                                                                                                                                                                          401
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                                               CGTGCGCCACGAAGAAGCGGCGGGCCTTCGCCGCGGGCGCCGAGTCCTACATCAGCGGACG
                                                                                       CGTTCGAAATGAGGAAGCGGCGGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGA 520
                                                                                                                                    CGGCGACACCCTCAACCATGTCACCGACGCCATCCATCGCAGCCAGATCCAGTGGGTCCA
                                                                                                                                                                              GGGTGACAGCCTTAATCCGATCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCA 460
                                                                                                                                                                                                                             CGCCGAGATCGTCGTGGAAACCCTGGAAGCCGCCGGCGGCGTCCGCCATTGCTATGGCATCGT
                                                                                                                                                                                                                                                                          CGCAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGT
    TCTCGGCGTGGTCGGCGACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCACCCTGATCCAGGTCGACCGCGATGGCAGTCACCTGGGCCGCCGCCACCCCATCGA
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                                                                                                                                                                                                                                                                                                                                                 7.6%;
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                                                                                                                                                                                                                                                                                                                                               Score 164.2; DB 4
Pred. No. 5.2e-41;
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                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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                                                                                                                                                                                                                                                                                                                                                                    Length 1113;
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; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-7166
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                                        NUMBER OF SEQ ID NOS:
SEQ ID NO 7166
LENGTH: 798
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7166, Application Patent No. 6551795
                                                                                                                                                                                                        FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
                                                                                                                          PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                         PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONITITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      880 CCTGACCGCCTGCGGCTCCTGCGGACCGGGCACCTGCACTTCATCAACGGCGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATTAAATCACCGATCGGGCATGCGCTGGGTAGAGAGCAGTACATCCAGCATGAGAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGACAACGTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAA 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCAAGGCGCCCATCGCGCACACGTCGCGGGCCAAGGACTTCGTCGAGTACGACAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCCACCATGGCGGGTAAAGGTGTGCTGGTAGTGATTCCTGGTGATATCGCTAAGGA 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCTGCGAGCAGGTGCACAGCCCGGGAACAGGCGCGCGGGGTGGTGGCCCTGGCCTGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTCGGCGTGGTCGGCGACGT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTATCCGGTGACCGGTGATGT 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCACCCTGATCCAGGTCGACCGCGATGGCAGTCACCTGGGCCGCCGCCACCCCATCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCAACATGGGCATGACCGGTATGCTCGGGATCGAGTCCGGCTTCCACATGATGACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGCGACGCCGAACTGCAGGACGTCGCCCGCCTGC - -TGGCCCACGGCAAGAAGATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCCACGGTGAAGGACGACCTGCCGTTCTCGGTGCATTTCCCGCAACCGGTGCTGCGCC
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US-09-107-532A-3181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3181, Application US/09107532A Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1441 CGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCGAGGT 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1381 ACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGG 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1561 CTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCG 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    644 AAGCCGGCAAGGGCGAGCTGATCCATCCGCAGCACCTGGTCAGCCTGCTCGACCAGCACG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCGGAGCTGGTGATGCCGCCGAAGATCGAGTTCGGCCAGGTC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTC 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCGGTGCAGGAGTTCCTCGCCCAGCCCGGTCCGGCGCTGCTGGACGTGCATACCAACC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGATATCGTCACGGATC 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAGAAAGTTCGCG 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAG 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAACTGCCGATCAAGGTAGTGGTGCTGAACAATGCCTCGCTGAACTTCGTCGAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCAACTICCGCTGAAGGCTGTGGGGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGATGTGTGGCGATGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGC 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAACGCCATGCCCCAGGCGCTGGGGGCTGAAGAAGGCCCTACCCCGAGCGCGCCAGGTGATCT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATCCACA - - - GCAACGGCAAGCGCCGCACCCTCACCAGCCTGGTCCACGGCACCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGGTTCATTCCGCCACGGCACGATGG 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGCGAGGACGCCCTGTTCACCGCCGACGGCGCCTCGGCGATGGTCTGGCTGTTGCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACAGAAGGTCGAGGGCCTGCTGGACAGCTACACCGACCTGCTCAACCCGGACTTCGCCC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGATCTCCGGCGACGGCCTGGCCATGCTGCTCGGCGACCTGCTGACGGCCATCCAGG 348
                                                                    APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                      STREET: 100 B
CITY: Waltham
                                                                                                                                                             OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                            SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                             100 Beaver Street
                                                                                                                                                                                                                                                                                          USA
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52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 798;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...1746; SEQUENCE DESCRIPTION: SEQ ID NO: 3181: US-09-107-532A-3181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3181:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1746 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                             437
734 GAATTATTCCTGATGATTATGAAAACTTTCTTGGTTTTGCTGGACGTGTCGCTACTAAAC 793
                                                                                           674 AAATCAAAGAATTCTCAGAACATTTTTCAGTTCCTGTTGTCGCTTCCGTTCTAGCAAAAG 733
                                                                                                                                                                                                                                                                                        554
                                                                                                                                                                                                                                                                                                                                                                                 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619 CTAGCCATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGA 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                559 CACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 CAGATGCAAAATTAACGGGGAAAGTCGGCGCTGTCTTCGGCTCTGCAGGACCTGGTGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              499 CGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTTCTTGTGGTCCTGGAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 AAACCGAAATCAACTACATTCAAGTTCGTCATGAAGAAGTCGGCGCACTCGCAGCCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 AATCAGATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGTTTTGCAGCCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGGACAAGTTGCTTCTACATCCATGAACTATAACTCTTTCCAGGAACTAAATGAAAATC 376
                                                                                                                                       AGGTGTTGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGCATGCGCTGGGTGGTAAGC 1038
                                                                                                                                                                                         TTGAAAAAGCAAAAAAACCAGTTCTTTATGTTGGTCAAGGAACGCGAAACGGATTTCCGC
                                                                                                                                                                                                                                     CTCACAAAACAAGTGTGATATTACCAGAAGAAAAAGATTTGCTAGCTGCTTTGCCTTATC
                                                                                                                                                                                                                                                                                                                                   CTTCTGGCACTCCTGTGGTGTTCCCCGGATCCTACTGAGGCTGCAGCCGCTGGTGGAGGCGA 918
                                                                                                                                                                                                                                                                                                                                                                                 TCCCTGTTGATCTTGGTTTTGAAGAAATTGACGAACAACCTTTCTCCA----CCGCTCACA 553
                                                                                                                                                                                                                                                                                                                                                                                                                               TTCCTGGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCCAATTCCACTATTT 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGTAGTAGATGAAGCCATTAAAGCCGCCTATGAGCATAAAGGCGTGGCTATCGTGACTA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTATTTTCGCAGATGTTAGCGTATACAATCGTACAGTCATGACACCACAAAGTCTTCCGC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGTGAGCAGGGTGAAC 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACATTTGATCAATGGTTTGTATGATGCACAGATGGACCATGTGCCTCTAGTAGCGTTCT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.1%; Score 110.2; DB 4; Length 1746; 44.2%; Pred. No. 4.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 803; Indels
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                                                                                                                                                                    Sequence 1619, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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; SEQ ID NO 1619
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1619
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                                                                         SEQ ID NO 8458
LENGTH: 2577
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                           Sequence 8458, Application Patent No. 6551795
GENERAL INFORMATION
                                                                                                                              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRIOR PRIOR DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
                                ORGANISM: Pseudomonas aeruginosa
-09-252-991A-8458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1348
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Best Local Similarity 45.5%;
Matches 773; Conservative
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CTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACA 1376
                                                                                                                                         GGTGCG------CACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGAT
                                                                                                                                                                                                                                                                       CTCGGCACCCGCGCCAGCAGCATGCTGATGGAGCATTGCGACACCCTGCTGATCGTCGGC
                                      GCAGGGGAAACCCTGGAGCGCCTGCTGCCGCTGCTCGAGCAGAAAAAGCACGGCGCCT--
                                                                     GTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAAACAGATCGTTCCTTC
                                                                                                                GACCTGTATCCGCGCAACATCGGTATCCGCTATCCGATCGACCAGGCCTTGCTCGGCGAT
                                                                                                                                                                                                                    ACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGTTGCCCAGGTGGATATCAAC
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                                                                                                                                                                                                                                                                                                                                               CTCCTGGGCAAGGCGGCTTTCCGACGACCTGCCGTACGTGACCGGCTCCATCGGCCTG
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                                                                                                                                                                                            GGCGCGCACCGGCAACTGGAAGCGGTCGCCGAGCGCCTGGCCGCCGGAGTGGCCAAGGCG
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1704

1205

1256

1145 1584 1085

1644

1025

1524

1464 965 1404 905 1344 1284 800 1224 1104

PRIOR FILING DATE: 1998-07-2: NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 8530 LENGTH: 2754 TYPE: DNA ORGANISM: Pseudomonas aerugin S-09-252-991A-8530 Query Match Best Local Similarity 45.5%; Matches 773; Conservative	CSCLEEN	ESULT 8 S-09-252-991A-8530 Sequence 8530, Application US/0925; Patent NO. 6551795 GENERAL INFORMATION: APPLICAMP: Marc T Rubenfield of	OY 1890 GGACCTGTACTGATCGATATCGTCACGATCCTAATGCGCTGTCGATCCACCAACCA	2 1 2 1 1	QY 1677 CTGCACCHACTCCGCTGAAGGCTAACTGGTCAACAGAGT 1718 Db 2173 CAGCAGTACTGGCAGCTGGGAGCTGGGGGTGTTTAACAACAGT 1718 Db 2173 CAGCAGTACTGGCAGCTGGGAGCTCGGCGACCTTCATCGTGGTGCTGGTGAACAACAGC 2232 QY 1719 TCTTTGGGCATGGTGAAGTTGGAAGTGCTCGTGGAGGAGAGTTTGGTACT 1775	1996 GGGACATCCGCATGCGCCATGCTCGGCTCGCTGTCGGGCAAACCTGGCGACC 1557 ATGGCTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTG	Db 1823GCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGG
Db Oy	Ду Ду Ду	Ф Ф Ф	Db Qy Db	0 D	0 D D D D D D D D D D D D D D D D D D D	Qy Db Qy Db	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
1206 GGTGCGCACATTGGTCGACGTACACGGTGAAGTATCCGGTGACCGGTGAT 1256		966 AATGCTCGCGCGCAGGTGTTGGAGGTTGGCGAGAAGATTAAATCACCGATCGGCCATGGC 1025	CGACGCCGACCTGGAGGCC CTGCGGTGCGGGCGTGAAG	### ##################################			327 ATGGCACACAGCTACGCAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGA 386

24:

CR-9989

0;

Mismatches 108;

0,

Gaps

650

81

141

201

21

Score 87.2; DB 3; Pred. No. 2.7e-17;

Length 260; Indels

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RESULT 9
US-08-735-545-24/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Van Dyk, T
APPLICANT: LAROSSA, R
TITLE OF INVENTION: A
TITLE OF INVENTION: P
NUMBER OF SEQUENCES:
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50
COMPUTER: IBM PC COMPUTER:
COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTE
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ADDRESSEE: E. I. DU PONT DE
                                                                                                CURRENT APPLICATION DATA:
                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDOWS SOFTWARE: MICROSOFT WORD 2.0C
                                                                                                                                                                                                                                                                                                                                     STREET: 1007 MARK
CITY: WILMINGTON
                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                    STATE:
                           CLASSIFICATION:
                                                       FILING DATE:
                                                                                                                                                                                                                                                                                      COUNTRY:
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A Facile Method for
Identifying Regulated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
ATTORNEY/AGENT INFORMATION: NAME: FLOYD, LINDA A.
                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: DISKETT
                                                                                                                                    CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Van Dyk, APPLICANT: LaRossa,
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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LENGTH: 260 base pairs
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                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT W.
SOFTWARE: MICROSOFT WORD 2.0C
                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         STREET: 1007 MARI
                                                                                                                                                                                                                                                                                                                       COUNTRY:
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REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN:
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US-09-252-991A-8318
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; ORIGINAL SOURCE:
; STRAIN: dpd35
US-09-449-083-24
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                                                                                                                                                                                                                                               SEQ ID NO 8318
                                                                                                                      Matches
                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8318, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                ENGTH: 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112
                                                                                                                    Local Similarity
mes 207; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 58.9 ses 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 302-773-0164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
387 ATTTATGGTTTGGTGGGTGACAGCCTTAATCCGATCGTGGATGCTGT-----CCGCCAA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 ACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140
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                                              ATGTCCAGCACGGTTGCCGATCAATTGCTCGAACGCTTGAGCCAGTGGGGGGGTGAAGCGC
                                                                            ATGCCACACAGCTACGCAGAACAATTAATTGACACTTTTGGAAGCTCAAGGTGTGAAGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTATTTCCAGGAAACCCCACCACAAGAGCTATTCCGCGAATGTAGTCACTATTGCGAG
                                                                                                                                                                                                                                                                                                                                                                                 MARC J. Rubenfield et al.

VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dpd3509 lower
                                                                                                                    Conservative
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                                                                                                                                 Score 81.2; DB 4;
Pred. No. 5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 87.2; DB 3;
Pred. No. 2.7e-17;
0; Mismatches 108;
                                                                                                                 Mismatches
                                                                                                                 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108;
                                                                                                                                             Length 1443;
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                                                                                                                 Indels
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RESULT 12
US-08-452-075-1
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                                                                                                                                                   TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION UMBER: 08/452,075
REFERENCE/DOCKET NUMBER: 10-741.
TELECOMMUNICATION INFORMATION:
                                         FEATURE:
                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 116340/1994
FILING DATE: 30-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: L-ISOLEUCINE-PRODUCING BACTERIUM AND
TITLE OF INVENTION: METHOD FOR PREPARING L-ISOLEUCINE TH
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 26-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: Patentin Release #1.0, Version #1.30
                    NAME/KEY:
                                                                            TOPOLOGY:
                                                                                           STRANDEDNESS:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON STATE: VIRGINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                      CENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 GGCCAGCAGGCGGCTACCGCGTTGGGCAGCGACTACCAGCAGGAAGTCGATCTGCAGAGC
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                                                                                                                nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08452075
                                                                                                                                  2841 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: OBLON, SPIYAK, MCCLELLAND, MAIER & NEUSTADT 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KISHINO, HIROKO
TSUJIMOTO, NOBUHARU
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                                                                        linear
                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/08/452,075
26-MAY-1995
                                                                                             double
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US-09-231-061-1
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Best Local Similarity
Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09231061 Patent No. 6214591 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHODS FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                          COUNTRY:
ZIP: 22
                                                                                                                                                                                                                                                                                                     STREET: 1755 S. CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFF. DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1443 GGACGCACTGTTAGATTCCATCCCTGTTGTTGCCATCACCGGTCAAGTGTCCGCACCGTT 1502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    581 TGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCA 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 CGTTCGAAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGA 520
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HASHIGUCHI, KENICHI
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KURAHASHI, OSAMU
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1195..2838
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    US/08/793,441
                                                                                      us/09/231,061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-FEB-19
APPLICATION NUMBER: PG
FILING DATE: 30-AUG-19
FRIOR APPLICATION DATA:
APPLICATION NUMBER: JI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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LOCATION: 2395..2400
OTHER INFORMATION: /note= "CLEAVAGE SITE:
OTHER INFORMATION: IDENTIFICATION METHOD:
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TELEPHONE: /vj.
TO TO NO:
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                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: OTHER INFORMATION:
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LOCATION: 119
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LOCATION:
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STRAIN: MI162
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1443 GGACGCACTGTTAGATTCCATCCCTGTTGTTGCCATCACCGGTCAAGTGTCCGCACCGTT 1502
                                                                                                                                      1323 ATGCCGACATGAGCAGGGTGCGGCAATGGCGGCTATCGGTTATGCTCGTGCTACCGGCAA 1382
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                                 581 TGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCA 640
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                                                                                                 2841 base pairs
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957.
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30-AUG-1994
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Pred. No. 1.7e-08;
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; OTHER INFORMATION: cleavage site (KpnI)
US-09-011-762-5
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US-09-011-762-5
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Best Local Similarity
Matches 209; Conserv
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APPLICANT: KISHINO, Hiroko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACID FILE REFERENCE: 0010-0911-0PCT CURRENT APPLICATION NUMBER: US/09/011,762 CURRENT FILING DATE: 1998-04-17 EARLIER APPLICATION NUMBER: PCT/JP96/02399 EARLIER FILING DATE: 1996-08-27 NUMBER OF SEQ ID NOS: 11
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APPLICANT: KURAHASHI, Osamu
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NAME/KEY: misc_feature
'COATION: (2395)...(240
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LOCATION: (52)...(57)
OTHER INFORMATION: cleavage site (SmaI)
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LOCATION: (957)..(1055)
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                                  CGTTCGAAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGA 520
                                                               ATGCCGACATGAGCAGGGTGCGGCAATGGCGGCTATCGGTTATGCTCGTGCTACCGGCAA
                                                                                                                           GTCCACCATGGCGGGTAAAGGTGTGTCGGTGGTAGT 796
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                                                                                                                                                                                                                                                    Score 60.8; DB 4;
Pred. No. 1.7e-08;
0; Mismatches 247;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25002 base pai.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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Sequence 48, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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MEDIUM TYPE: Diskette,
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                                          6377 CAGGAACACTCAGCTCATTGATGGACGCTTTGGCTGAAGACAAAGATATCCGTTTCTTAC
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460 ACGTTCGAAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGG 519
                                                                                       403 GTGACAGCCTTAATCCGATCGTGGATGCTGTCCGCCAA---TCAGATATTGAGTGGGTGC 459
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                                                                   6017 GTGCTGCAGTTTCTAAAAAAGGTCCAGCTGTTGTTGAAATTCCAGTAAACTTCGGTTTCC 5958
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                                                                                       760 AGTCCACCATGGCGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGG 819
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                                820 AAGACGCAGGTGACGGTACTTATTCCAATTC 850
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Search completed: October 3, 2003, 18:52:48 Job time: 164 secs

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OM nucleic -
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Scoring table:	Title: Perfect score: Sequence:
IDENTITY_NUC	US-09-965-825-1 2160 1 ttagaggcgattctgtgagg

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Gapop 10.0 , Gapext 1.0

2552756 seqs, 1349719017 residues

Minimum DB Maximum DB seq length:
seq length: 0 20000000000

Total number of hits satisfying chosen parameters:

5105512

Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: //SIDSI/gcgdata/genesed/genesedn-embl/NA1889_DAT: *
2: //SIDSI/gcgdata/genesed/genesedn-embl/NA1899_DAT: *
2: //SIDSI/gcgdata/genesed/genesedn-embl/NA1991_DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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Corynebacterium gl

Corynebacterium Nucleotide sequenc C. glutamicum ATCC

Corynebacterium

Corynebacterium gl

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glutamicum pyru

ALIGNMENTS

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Genomic sequence o

Pseudomonas aerugi

Listeria innocua c Listeria innocua D Bacillus lichenifo

Listeria monocytog

Human ORFX polynuc Human ORFX polynuc Staphylococcus aur Staphylococcus aur Staphylococcus aur Escherichia coli p Escherichia coli p

Pathogen specific DNA encoding novel

RESULT 1 AAS15847 AAS15847 standard; DNA; 2160 BP

AAS15847;

16-JAN-2002 (first entry)

C. glutamicum gene for pyruvate oxidase, poxB.

Transketolase; tkt; ds; L-amino acid fermentation; animal nutrition; human medicine; pharmaceutical industry; pyruvate oxidase; poxB.

Corynebacterium glutamicum

CDS Location/Qualifiers 327..2066 'product= "Pyruvate oxidase"

20-SEP-2001.

WO200168894-A1.

05-JUL-2000; 2000WO-EP06305

17-MAR-2000; 2000US-0528196.

(DEGS) DEGUSSA AG. (UYNA-) UNIV NAT IRELAND.

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Matches 2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid pEC-T18mob2 which contains the tkt gene. The method is useful for the fermentative preparation of L-amino acids, i.e. L-lysine, L-threonine and L-isoleucine, in which at least the tkt gene is amplified. L-lysine, L-threonine and L-isoleucine are useful in animal nutrition, in human medicine and in the pharmaceuticals industry. The present sequence is the gene for pyruvate oxidase, poxB, which was eliminated by mutation in a strain expressing with tkt in order to further increase yields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the preparation of L-amino acids of fermenting L-amino acid-producing coryneform bacteria which overexpresses a gene e.g. that for transketolase, tkt. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of L-amino acids, e.g. L-lysine, L-threonine or L-isoleucine, useful in animal nutrition or in human medicine, comprises fermenting L-amino acid-producing coryneform bacteriamplification of the tkt gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                included are transformed coryneform microorganisms harbouring
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    Preparing L-amino acids by fermenting coryneform bacteria transformed with the glucose 6-phosphate dehydrogenase gene is particularly useful
                                                                                                           Stapelton
                                                                                                                                                     (DEGS ) DEGUSSA AG.
(KERJ ) FORSCHUNGSZENTRUM JUELICH
(UYNA-) UNIV NAT IRELAND.
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foodstuff industry; pyruvate oxidase; po
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                                                                                                     n H, Eggeling L, Moritz B,
Moeckel B, Thierbach G;
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 327..2066
                                                                                                                                                                                                                                                                                                                                             /product= "Pyruvate oxidase (poxB)"
                                                                                                                                                                                                                                                                                                                                                                 /*tag=
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                                            AGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATG
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The present invention relates to a method for preparing L-amino acids by fermenting coryneform bacteria, comprising fermenting the L-amino acid producing bacteria in which at least the glucose 6-phosphate dehydrogenase (zwf) gene is amplified, and concentrating and isolating the L-amino acid produced. The L-amino acids produced are used in animal nutrition, human medicine, foodstuffs industry and the pharmaceuticals industry. The present sequence is Corynebacterium glutamicum strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2160 BP; 491 A; 486 C; 647 G; 536 T; 0 other;
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                                                                         TTAGAGGCGATTCTGTGAGGTCACTTTTTGTGGGGTCGGGGTCTAAATTTGGCCAGTTTT
                  AAGCGTGGCAACAATTTAAGAGCACAATTGAAGTCGCACCAAGTTAGGCAACAC
                                                                                                                                                             TIGGTTTCGACGGGCTGAAACCAAACCAGACTGCCCAGCAACGACGGAAATCCCCAAAAGT
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AAGCGTGGCAACAACTGGAATTTAAGAGCACAATTGAAGTCGCACCAAGTTAGGCAACAC
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CGATGTGTGGCGATGGTTGTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGC
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                                                                                      AGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAGAAAGTTCGCG
                                                                                                                                    AGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAGAAAGTTCGCG
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Sequence 2160 BP;

animal nutrition, human medicine and the pharmaceuticals industry.

491 A; 486 C; 647 G; 536

T; 0 other

δõ Дb γ Вb δÃ 밁 Qγ Db QΥ B

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                                                                                The present sequence represents the poxB gene of Corynebacterium glutamicum. The poxB gene encodes a pyruvate oxidase enzyme. The poxB gene and the gnd gene are used to produce recombinant bacteria for use in the course of the invention. The gnd gene encodes a 6-phosphogluconate dehydrogenase enzyme. The specification describes a method for the fermentative preparation of L-amino acids, in
                                       particular L-lysine, L-threonine, and L-tryptophan. The method comprises fermenting coryneform bacteria in which at least the gnd gene is amplified and overexpressed. The L-amino acids produced are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum
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                                                                                                                                                                                         Example 9; Page 47-50; 59pp; English.
                                                                                                                                                                                                                      to produce L-lysine and L-threonine
                                                                                                                                                                                                                                     Preparing L-amino acids by fermenting coryneform bacteria transformed with the 6-phosphogluconate dehydrogenase gene is particularly useful
                                                                                                                                                                                                                                                                                   P-PSDB; AAG79096
                                                                                                                                                                                                                                                                                                                             Dunicau LK, McCormack A,
                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2000; 2000US-0531265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of the Corynebacterium poxB gene
                                                                                                                                                                                                                                                                                                                                                        (DEGS ) DEGUSSA AG.
(UYNA-) UNIV NAT IRELAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; 6-phosphogluconate dehydrogenase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCGGTGCCCATGAGATTGCCCT 2160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-tryptophan; poxB gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-EP06299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "pyruvate
                                                                                                                                                                                                                                                                                                                           Stapelton C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyruvate oxidase;
                                                                                                                                                                                                                                                                                                                             Burke K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-amino acid; L-lysine;
                                                                                                                                                                                                                                                                                                                              Moeckel
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2	Query M Best Lo Matches Qy Db Qy Db Qy Db Qy Db Qy Db
OI AATHGCCATAACGTTGAAGGATTCAGATGCCACACCTAGCTGAACAACTACTAGCAAATTGACA OI AATHGCCATAACGTTGAAGGAGTTCAGATGCCACACCTACACCAACAACTACTACACAAACAA	Match Local S 20 2160 1 1 61 61 121 121 181 181 181 241
1381 AGGTGAGAACCATGTCCCTATTCACCCTGAATACCTTCCTCTATTTTGAACCAGCTGG 1441 CGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCATGTTTTGAACCAGCTGG 1441 CGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTTGGCATGCAGGT 1501 ACATCGAGAATCCGGAGGAAGGAACGCGCAACTTTGTGGCATTCGCAATGTTGGCATGCGAGGT 1501 ACATCGAGAATCCCGAAGGAACGCGCGACTTTGTGGGTTCATTCGCCACGGCACGTGGGATGGGATGGGATGGGATGGGATGCGAGGT 1501 ACATCGAGAATCCCGAAGGAACGCGCGACTTTGTGGGTTCATTCGCCACGCCACGTGGGT 1501 ACATCGAGAATCCCGAAGGAACCGCGAACTTTGTGGGTTCATTCGCCACGCCACGTGAGG 16111111111111111111111111111111111	

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RESULT 4
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Best Local 9
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                                                                                                                                                                                especially animal nutrition. (I) is also useful as a source of probes and primers for isolation of related sequences. Cells in which the poxB gene is suppressed produce higher yields of L-amino acids. This sequence encodes the pyruvate oxidase (E.C. 1.2.2) poxB gene from Corynebacterium glutamicum ATCC13032 which is described in the invention.
                                                                                                                                                                                                                                                          This invention describes a novel polynucleotide (I) which is used for insertional mutagenesis of the poxB gene in coryneform bacteria. The poxB gene can be used for fermentative production of L-amino acids, specifically L-lysine, which is used in human medicine, foods and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. glutamicum ATCC13032 poxB DNA.
                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 13-16; 21pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
-35_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyruvate oxidase; poxB; E.C. 1.2.2.2; mutagenesis; coryneform bacteria; fermentation; L-amino acid production; L-lysine production; medicine;
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                                                                                                                                                     Sequence 2160 BP; 491 A; 486 C; 647 G; 536 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moeckel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1999;
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                                                TTAGAGGCGATTCTGTGAGGTCACTTTTTGTGGGGTCGGGGTCTAAATTTGGCCAGTTTT
    CGAGGCGACCAGGCGTGCCCACGATGTTTAAATAGGCGATCGGTGGGCATCTGTGT
                                   TTAGAGGCGATTCTGTGAGGTCACTTTTTGTGGGGGTCGGGGTCTAAATTTGGCCAGTTTT
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/note= "As given in the specification"
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                                                                                                      100.0%; Score 2160; 100.0%; Pred. No. 0;
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Corynebacterium poxB encoding polynucleotide SEQ ID

NO

05-JUL-2002 (first entry)

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Best Local Similarity
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-35_signal
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                                                                                                                                                                                                                                                                                                                               acid (I) by growing a (I)-producing coryneform bacterium in which the activity of at least the sequence poxB (ABLS9754, ABLS9756) encoding pyruvate oxidase (ABB59755, EC 1.2.2.2) has been weakened, especially switched off. (I) is then recovered from medium or cells. (I) is a vitamin useful in human medicine, the pharmaceutical and food industries and particularly in animal nutrition. Reducing the activity of poxB
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Page 11-14; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fermentative production of D-pantothenic acid (1), useful e.g. in animal nutrition, from coryneform bacteria with reduced activity cyruvate oxidase gene \,
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P-PSDB; ABB79447.
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                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the fermentative production of D-pantothenic
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ABL58756 standard; DNA; 3248 ВP

05-JUL-2002 (first entry)

Corynebacterium poxB encoding polynucleotide SEQ ij ĕ

Corynebacterium; poxB; pyruvate oxidase; p-pantothenic acid; vitamin; medicine; p animal nutrition; gene; ds. pharmaceutical; enzyme; fermentative food ve production; industry;

Corynebacterium glutamicum

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fermentative production of D-pantothenic acid (I), useful e.g. in animal nutrition, from coryneform bacteria with reduced activity pyruvate oxidase gene
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3248 BP; 744 A; 743 C; 985 G; 776 T; 0 other;
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07-APR-2000;
03-AUG-2000;
     Novel polynucleotides derived from Coryneform bacteria, mutation point of a gene, measuring expression of a gene
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expression profile or pattern of a gene and identifying homologous gene

Disclosure; SEQ ID NO: 7068; 246pp + Sequence Listing; English.

from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived analysing the general pattern of a gene derived analysing the general pattern of a gene derived analysing the gener The present invention provides a number of nucleotide and protein

Sequence 349980 BP; 81250 A; 97718 C; 90621 G; 80391 T; 0 other;

European Patent Office.

밁 Qy δÃ δÃ рь Ş 망 γQ 밁 Qy 20 В Ş B δÃ Вb Qy 밁 В δÃ DЬ B VQ. Query Match Best Local Similarity Matches 2160; 78290 78410 78710 TTGGTTTCGACGGGCTGAAACCAAACCAGACTGCCCAGCAACGACGGAAATCCCAAAAGT 78830 TTAGAGGCGATTCTGTGAGGTCACTTTTTGTGGGGTCGGGGTCTAAATTTGGCCAGTTTT 7877] 241 AAGCGTGGCAACAACTGGAATTTAAGAGCACAATTGAAGTCGCACCAAGTTAGGCAACAC 121 TTGGTTTCGACGGGCTGAAACCAAACCAGACTGCCCAGCAACGACGGAAATCCCAAAAGT 1 TTAGAGGCGATTCTGTGAGGTCACTTTTTGTGGGGGTCGGGGTCTAAATTTGGCCAGTTTT CGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCC CTTGTGGTCCTGGAAACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTG CTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTG CGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTTG CGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTT TCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGG TCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGG AAGCGTGGCAACAACTGGAATTTAAGAGCACAATTGAAGTCGCACCAAGTTAGGCAACAC Conservative 100.0%; 100.0%; 0; Mismatches Score 2160; Pred. No. 0; DB 22; 0; Indels Length 349980; Gaps 120 720 660 600 540 480 420 78471 300 240 180 60 7829 78531 78651 78711 78351 78411 0;

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                                                                                          AGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAG
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GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCGGTGCCCATGAGATTGCCCT
                                          GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCGGTGCCCATGAGATTGCCCT 2160
                                                                                ACATAAGGAATATTCCTACTCCATGATGATGATACACCTGCTGTTCTCATTGACCGCGA
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AAF71402 standard; DNA; 1860 ВP

30-APR-2001 (first entry)

Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:85

RESULT 8
AAF71402
ID AAF7
XX XX
AC AAF7
XX AAF7
XX COTY
XX COT Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.

Corynebacterium glutamicum

WO200100844-A2

04-JAN-2001.

23-JUN-2000; 2000WO-IB00943.

08-JUL-1999; 08-JUL-1999; 08-JUL-1999; 08-JUL-1999; 08-JUL-1999;

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08-JUL-1999; 08-JUL-1999; 08-JUL-1999; 09-JUL-1999; 09-JUL-1999; 99DE-1031434. 99DE-1031510. 99DE-1031562. 99DE-1031634. 99DE-1032180. 99DE-1032227. 99DE-1031428. 99DE-1031431. 99DE-1031433.

99DE-1032230 99US-0143208 99UE-1032924 99DE-1032973 99DE-1032973 99DE-1032065 99DE-1040765 99DE-0151572 99DE-1042076.

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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1860 BP; 426 A; 405 C; 562 G; 467 T; 0 other;
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                                                            AGTATGTGCTGCTTCTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTC
                                                                                          AAATGAGGAAGCGGCGCTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAAGCTGGC
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sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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Tateishi N,
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                                                                                                                                                                                                                                                      8; SEQ ID NO: 2873; 246pp + Sequence Listing; English.
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Senoh A, Ikeda M, Ozaki A;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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compound;
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polyketide;
                                                                                                                                                                                                                              ID NO:89
   enzyme;
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                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; Corynebacterium diphtheriae; evolutionary study;
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(BADI) BASF AG.

Pompejus M, Kroeger 'n Schroeder H, Zelder Ó Haberhauer

P-PSDB; 2001-061975/07. AAB79287

New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, modulation of production carbohydrates or enzymes Ö,

Claim 3; Page 274-275; 1246pp; English.

CC energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of corporation of fine chemicals, such as, an organic acid, a proteinogenic corporation of the production of the production of the proteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty control of a carbohydrate, an aromatic compound, a vitamin, a carbohydrate, an aromatic compound, a vitamin, a confector, a polyketide, or an enzyme. The presence of (I) or SMP proteins (II) encoded by them are used for diagnosing the presence or activity of corganization of them are used to map genomes of organization related to containing them are used to map genomes of organizations required to containing them are used to map genomes of organizations required in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production coin a cell (i.e. ATP, NADPH). metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POCET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1683 CAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTTGGAG
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                                                                                                                                                                                                                                                                      1863 CAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGATATCGTCACGGATCCT 1922
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901
                                                                                                                                                      781 AATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCATGGGATTCAGCAAGGCG
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                                                                                               ATGCTCGTGGAGGGACAGCCAGAATTTGGTACCTGACCATGAGGAAGTGAATTTCGCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTGTGGCGATGGTGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGCAC 1682
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ATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT 944
                                     ATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT 2086
                                                                          AATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCATGGGATTCAGCAAGGCG 1982
                                                                                                                                                                                                                                 CAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGATATCGTCACGGATCCT
                                                                                                                                                                                                                                                                                                               ATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAGAAAGTTCGCGAG
                                                                                                                                                                                                                                                                                                                                                ATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAGAAAGTTCGCGAG 1862
                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAGAG 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGGAG
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the preparation of L-amino acids comprising fermenting L-amino acid-producing coryneform bacteria which overexpresses a gene e.g. that for transketolase, tkt. Also included are transformed coryneform microorganisms harbouring the plasmid pEC-T18mob2 which contains the tkt gene. The method is useful for the fermentative preparation of L-amino acids, i.e. L-lysine, L-threonine and L-isoleucine, in which at least the tkt gene is amplified. L-lysine, L-threonine and L-isoleucine are useful in animal nutrition, in human medicine and in the pharmaceuticals industry. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is a fragment of the gene for pyruvate oxidase, poxB, which was used to eliminate the poxB gene by insertional mutagenesis in a strain expressing with tkt in order to further increase yields of L-amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. glutamicum pyruvate oxidase, poxB, mutagenic fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amplification of the tkt gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprises fermenting L-amino acid-producing coryneform bacteria with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of L-amino acids, e.g. L-lysine, L-threonine or L-isoleucine, useful in animal nutrition or in human medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656800/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human medicine; pharmaceutical industry; pyruvate oxidase; poxB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transketolase; tkt; ds; L-amino acid fermentation; animal nutrition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thierbach G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunican LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYNA-) UNIV NAT IRELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DEGS ) DEGUSSA AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200168894-A1.
945 TTCTGCGGTGCGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATT 1004
                                                                         885 GATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTG
                                                                                                                                                                                                                                                                                                                705 TGCGAGATGGTGAATGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC
                                     181 GATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTG
                                                                                                                                                                                                                                       765 ACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC 824
                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                             1 TGCGAGATGGTGAATGGTGGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                 ACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC 120
                                                                                                                                                       GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 884
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCormack A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                         40.5%; Score 875; DB 22; Length 875; 100.0%; Pred. No. 7.7e-269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stapelton C,
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burke K,
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 12
AAD20204
ID AAD20
XX AAD20
AC AAD20
XX O3-JAI
XX L-amii
XX L-amii
XX Godyn
XX Gooryn
XX Hoods
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                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                    L-amino acid; fermentation; coryneform bacteria; animal nutrition; glucose 6-phosphate dehydrogenase; zwf; human medicine; foodstuff industry; pyruvate oxidase; poxB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD20204 standard; DNA; 875
                             (DEGS ) DEGUSSA AG.
(KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH
(UYNA-) UNIV NAT IRELAND.
                                                                                                                                          20-MAR-2000; 2000US-0531269.
                                                                                                                                                                                           05-JUL-2000; 2000WO-EP06303.
                                                                                                                                                                                                                                                                                                           W0200170995-A1
                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical industry; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR product of C. glutamicum poxB internal fragment DNA.
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Matches 875;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fermenting coryneform bacteria, comprising fermenting the L-amino acid producing bacteria in which at least the glucose 6-phosphate dehydrogenase (zwf) gene is amplified, and concentrating and isolating the L-amino acid produced. The L-amino acids produced are used in animal nutrition, human medicine, foodstuffs industry and the pharmaceuticals industry. The present sequence is the PCR product of Corynebacterium glutamicum strain ASO19 pyruvate oxidase (poxB) internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparing L-amino acids by fermenting coryneform bacteria transformed with the glucose 6-phosphate dehydrogenase gene is particularly useful to produce L-lysine and L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burke K, Sahm H,
Stapelton C, Moe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 875 BP; 190 A; 193 C; 266 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for preparing L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Page 59-60; 63pp; English.
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                                                                                                                                                                             GTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACA 130
GAGACGTACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT
                                                 GATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA 660
                                                                                                  GATCGTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA 136
                                                                                                                                                                                                                                                         GTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCG 540
                                                                                                                                                                                                                                                                                                                                                          GATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTAAAGACAAC 480
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                                                                                                                                                                                                                                                                                                                                                                                                              GAGGTCGGCATGTCTGGCCTGGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCG 420
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                                                                                                                                                       GTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCG 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTGCGGTGCGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAAGTTGGCGGAGAAGATT 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCGAGATGGTGAATGGTGGGGGGGGGGGGGGGGGGATTTGCATCACGCGATTCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 100.0%; Pred. No. 7. Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eggeling L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 875; DB 22;
; Pred. No. 7.7e-269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunican LK,
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RESULT 13
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ID AAI65
XX AAI65507
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XX DT 10-DE
XXX GNC1(
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QΥ
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                                                                                                                                                                                                             Matches 875;
                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a fragment of the poxB gene of Corynebacterium glutamicum. The poxB gene encodes a pyruvate oxidase enzyme. The poxB gene and the gnd gene encodes a pyruvate oxidase enzyme. The for use in the course of the invention. The gnd gene encodes a phosphogluconate dehydrogenase enzyme. The specification describes a method for the fermentative preparation of L-amino acids, in particular L-lysine, L-threonine, and L-tryptophan. The method comprises fermenting coryneform bacteria in which at least the gnd gene is amplified and overexpressed. The L-amino acids produced are used in animal nutrition, human medicine and the pharmaceuticals industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparing L-amino acids by fermenting coryneform bacteria transformed with the 6-phosphogluconate dehydrogenase gene is particularly useful to produce L-lysine and L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gnd gene; 6-phosphogluconate dehydrogenase; L-amino acid; L-lysine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                   Sequence 875 BP; 190 A; 193 C; 266 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-602792/68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2000; 2000WO-EP06299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 10; Page 52; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAR-2000; 2000US-0531265
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765 ACCATGGCGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC 824
                                                                                                                                                                                                                                              Similarity
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                                                                   TGCGAGATGGTGAATGGTGGTGAGCAGGTGAACGCATTTTGCATCACGCGATTCAGTCC
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McCormack A,
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                                                                                                                                                                                                                                   40.5%; Score 875; DB 22; 100.0%; Pred. No. 7.7e-269;
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                                    1545 CGCCACGCCACGATGCCTAATGCGTTGCCTCATGC 1579
                                                                                                                                                                                                 1425 ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAAT 1484
                                                                                                                                                                                                                                                           1365 GAGACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT 1424
                                                                                                                                                                                                                                                                                                                                                            1305 GATCGTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA 1364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1005 AAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 1064
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841 CGCCACGGCACGATGGCTAATGCGTTGCCTCATGC 875
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                                                                                                                                                                                                                                          GAGACGTACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT
                                                                                                                                                                                                                                                                                                                    GATCGTTCCTTCATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA 660
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                                                                            GTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTC
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RESULT 14
AAF61780
ID AAF61780
XX AAF61
XX AAF61
XX AF61
XX P71U
DT 27-JU
DT 27-JU
DY C-J1
XX PY1U
KW Ferme
KW ferme
KW Food
XX Coryn
XX Coryn
XX EP109

AAF61780 standard; DNA; 875 BP

27-JUL-2001 (first entry)

C. glutamicum ATCC13032 poxB DNA fragment from plasmid pCR2.1-TOPO.

Pyruvate oxidase; poxB; E.C. 1.2.2.2; mutagenesis; coryneform bacteria; fermentation; L-amino acid production; L-lysine production; medicine; food production; animal nutrition; ds.

Corynebacterium glutamicum

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel polynucleotide (I) which is used for insertional mutagenesis of the poxB gene in coryneform bacteria. The poxB gene can be used for fermentative production of L-amino acids, specifically L-lysine, which is used in human medicine, foods and especially animal nutrition. (I) is also useful as a source of probes and primers for isolation of related sequences. Cells in which the poxB gene is suppressed produce higher yields of L-amino acids. This sequence encodes a fragment of the pyruvate oxidase (E.C. 1.2.2.) poxB gene from corynebacterium glutamicum ATCC13032 found in plasmid pCR2.1-Topo which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 875 BP; 190 A; 193 C; 266 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 18; 21pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DEGS ) DEGUSSA AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform glutamicum poxB pyruvate oxidase insertional mutation, producing strains with
               1185 GTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCG 1244
                                                                                                                                                                       1065 GAGGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCG
                                                                                                                                                                                                                                               1005 AAATCACCGATCGGGCATGCGCTGGGTAGGTACATCCAGCATGAGAATCCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-309855/33
                                                                                                                                                 361 GAGGTCGGCATGTCTGGCCTGCGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCG
                                                                                                                                                                                                                                                                                                 241 TTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         825 GCAGGTGACGGTACTTATTCCAAATTCCACTATTTCTTCTTGGCACTCCTGTGGTGTTTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      705 TECGAGATEGTGAATEGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H
                                                                                                                                                                                                                                                                                                                                                                                               GATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCATGGCGGGTAAAGGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC
GTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCG
                                                                                                           GATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTAAAGACAAC
                                                                                                                                                                                                                         AAATCACCGATCGGGCATGCGCTGGGTGATAAGCAGTACATCCAGCATGAGAATCCGTTT
                                                                                                                                                                                                                                                                                                                                       TTCTGCGGTGCGGGGGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATT
                                                                                                                                                                                                                                                                                                                                                                           GATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCGAGATGGTGAATGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dusch N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99DE-1051975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.5%; Score 875; DB 22; 100.0%; Pred. No. 7.7e-269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfefferle W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Puehler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide useful 
increased production
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RESULT 15
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                                              The invention relates to the fermentative production of D-pantothenic acid (I) by growing a (I)-producing coryneform bacterium in which the activity of at least the sequence poxB (ABL58754, ABL58755) encoding pyruvate oxidase (ABB58755, EC 1.2.2.2) has been weakened, especially switched off. (I) is then recovered from medium or cells. (I) is a vitamin useful in human medicine, the pharmaceutical and food industries and particularly in animal nutrition. Reducing the activity of poxB improves fermentative production of (I). The present sequence is that of a polynucleotide fragment of the poxB gene, useful in examples of the
                                                                                                                                                                                                                                      Example 3; Page 16; 28pp; German.
                                                                                                                                                                                                                                                                           pyruvate oxidase gene
                                                                                                                                                                                                                                                                                           Fermentative production of D-pantothenic acid (I), useful e.g. in animal nutrition, from coryneform bacteria with reduced activity of
                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-363950/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-2000; 2000DE-1048604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2001; 2001DE-1017085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE10117085-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              animal nutrition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D-pantothenic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium; poxB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium poxB encoding polynucleotide fragment SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL58755 standard; DNA; 875 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCACGGCACGATGGCTAATGCGTTGCCTCATGC 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTC 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAAT 780
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                                                                                                                                                                                                                                                                                                                                                                                      Herrmann T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                           coryneform bacteria with reduced activity of the
                                                                                                                                                                                                                                                                                                                                                                                      Thierbach
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Sequence 875

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1005 AAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 1064
                                           1545 CGCCACGCACGATGGCTAATGCGTTGCCTCATGC 1579
                                                                                                                          1485 GTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGGTTCATTC 1544
                                                                                                                                                                                                              1425 ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAAT 148
                                                                                                                                                                                                                                                                                                                                                                                    1305 GATCGTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1185 GTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCG
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841 CGCCACGCACGATGCCTAATGCCTCATGC 875
                                                                                                                                                                          721
                                                                                                                                                                                                                                                                                                                                           601 GATCGTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA
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                                                                                                                                                                                                                                                         661 GAGACGTACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGCGAGATGGTGAATGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC
                                                                                                                                                                                                                                                                                                  GAGACGTACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT 1424
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                                                                                                                                                                     ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAAT
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Title: Perfect score: Database : Total number of hits satisfying chosen parameters: Searched: Scoring table: Sequence: Run on: OM nucleic - nucleic search, using sw model GenEmbl:*

1: gb_ba:*

2: gb_ha:*

3: gb_in:*

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gb_p1:* gb_ba:*
gb_htg:*
gb_in:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX137665	RESULT 1
Kalinowski,J., Bathe,B. and Dusch,N. Nucleotide sequence encoding corynebacterium poxb-gene and its use	Moeckel, B., Weissenborn, A., Pfefferle, W., Puehler, A.,	Corynebacterineae; Corynebacteriaceae; Corynebacterium.	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	Corynebacterium glutamicum	Corynebacterium glutamicum	•	AX137665.1 GI:14273850	AX137665		AX137665 2160 bp DNA linear PAT 30-MAY-2001		

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                                                   /protein_id="CAC93726.1"
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/db_xref="G::15984084"
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DIAKEDAADGTYSNSTISSGTPVYFPDPTEAAALVEAINNAKSYTLFCGGYKNARAQ
VLELAEKIKSPIGHALGGKQYTQHENPFEVGMSGLLGYGACVDASNEADILIILLGTDF
PYSDFLPKDNVAQVDINGAHIGRRTTVKYPVTGDVAATIENILPHVEEKTDRSGFLDRM
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LHQLPLKAVVFNNSSLGMVKLEMLYEGGPEFGTDHEVKNFAEAAAGIKSVAITDPK
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DLARSNIRNIPTP"
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                                   TGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCCGGAGAAGATTAAATCACCGATCGGGC
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                                                                                                                                                     ATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGGATCCTACTGAGGCTG
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DIAKEDAGGGTYSNSILSSGTPVVFPDPTEAAALVEAINNAKSVYLFCGAGVKNARAQ
VLELAEKIKSPIGHALGGKOYIQHENPFEVGHSGLLGYGACVDASNEADLLILGTDF
PYSDFLPKDNVAQVDLNGAHIGRRTTVKYPVFGDVAATIENILPHVKEKTDRSFLDRM
LKAHERKLSSVVETYTHNVEKHYPIHPSYVASILNELADKDAVFTVDTGKONVHHARY
IENPEGTRDFYGSFRHGTMANALPHAIGAQSVDRNRQVIAAGCGOGGLGMLGELITVK
LHQLPLKAVVFNNSSLGMVKLEMLVEGQPEFGTDHEEVNFAEIAAAAGIKSVRITDPK
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AX253251
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                                                                  Degussa AG (DE); FORSCHUNGSZENTRUM University of Ireland (IE)
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/organism="Corynebacterium/mol_type="genomic DNA"
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                                                                               AGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATG 720
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LHQLPLKAYVENNSSLGMVKLEMLYEGQPEFGTDHEEVNFAEIAAAAGIKSYRITDPK
KVREQLAEALAYPGPYLIDIYTDPNALSIPPTITWEQVMGFSKAATRTYFGGGYGAMI
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                                                                                                   AGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAG
                                                                                                                                                            ACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG
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Query Match 100.0%; Score 2160; DB 6; Length 2160; Best Local Similarity 100.0%; Pred. No. 0; Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 1 Tragaggggartttgggggtctggggtctgaaattttggccagftt 60	-35_signal 227. 232 -10_signal 256261 256261 256266 /note="unnamed protein product" /codon_start=1 /protein_id="cansile=11 /protein_id="cansile=11 /protein_id="cansile=11 /protein_id="cansile=11 /protein_id="cansile_10" /db_xref="GI:21437889" /translation="MAHSYABCLIDTLEAQGVKRIYGLVGDSLNPIVDAYROSDIEWV HVRNEEAAAFAGAESLITGELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIP SAQIGSTFROETHPEILFKECSGYCEMVNGEGQGERILHHAIQSTMAGKGYGVVVIPG DIAKEDAGDGTYSNSTISSGTPVVFPDPTEAAALVEAINNAKSYLFCGACVKNARAQ VLELAEKIKSPIGHALGGKGYIQHENDFEVGMSGLLGYGACVDASNEADLLILLGTDF PYSDFLFKONVAQVDINGAHIGRRTTVKPVTGDVAATIENILPHVKEKTDRSFLDRM LKAHERKLSGVVETYTHNVEKHVFIHPEYVASILNELADKDAVFTVDTGMCNVHARY IENPEGTROFVGSFHGTMANALFHAIGAGSVDRNAQVIANGCDGGIGMLLGELLTVK LHQLPLAXVVENNSSLGMVKLEMLYEGQDEFGTDHEEVNRAEIAAAGIKSVRITPDFK KVREQLAEALAYPGPVLIDIVTDPNALSIPPTITWEQVMGFSKAATRTVFGGGVGAMI DLAASNIRMIPTP" BASE COUNT 491 a 486 c 647 g 536 t	SULT 5 404607 AX404607 AX404607 AX404607 CESSION AX404607 AX404607 AX404607.1 GI:21437888 Corynebacterium glutamicum ORGANISM Corynebacterium glutamicum ORGANISM Corynebacterineae; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium. TITLE Corynebacterineae, Corynebacteriaceae; Corynebacterium. 1 AUTHORS Dusch, N., Herrmann, T. and Thierbach, G. TITLE Process for the fermentative preparation of D-pantothenic acid using Coryneform bacteria using Coryneform bacteria DEGUSSA (DE) Location/Qualifiers DEGUSSA (DE) J. 2160 Jorganism="Corynebacterium glutamicum" Jmb_type="genomic DNA" Jmb_type="genomic DNA"	Db 1801 AGATTGCGGCGGCTGCGGTATCAAATCGGTACGCATCACAGATATCCGAAGAAAGTTCCCG 1860 Qy 1861 AGCAGCTAGCTGAGGCATTGGCATATCCTGACCTGATCGATATCGATCACAGATC 1920
Oy 1021 ATGCGCTGGGTGAGTAACCAGTACAGCATGAGAATCCGTTTGAGGTCGGCATGTCTG 1080	Qy 721 GTGGTGAGCAGGTGAACGCATTTTGCATCAGGCATTCAGTCACCATGGCGGTAAAG 780	361 CTTTGGAAGCTCAAGGTGTAAGCGAATTTATGGTTTGGTTGACAGCCTTAATCCGA	Db 1 TTAGAGGCGATTCTGTGAGGTCACAGAGTTTAAATAGGCGATCGGTGGCAGCAAAGT 120 61 CGAGGCGACCAGACAGGCGTGCCCACGATGTTTAAATAGGCGATCGGTGGCATCTGTGT 120 61 CGAGGCGACCAGACAGGCGTGCCCACGATGTTTAAATAGGCGATCGGTGGCATCTGTGT 120 61 CGAGGCGACCAGACAGGCGTGCCCACGATGTTTAAATAGGCGATCGGTGGGATCTGTGT 120 61 CGAGGCGACCAGACAGGCGTGCCCACGATGTTTAAATAGGCGATCGGTGGGATCTGTGT 120 62 CAGGCGACCACACACAAACCAAACCAGACTGCCCAGCAACGAAGT 180 121 TTGGTTTCGACGGCTGAAACCAAACCAGACTGCCCAGCAACGAACTCCCAAAAGT 180 122 TTGGTTTCGACGGGCTGAAACCAAACCAGCACGACAACTCCCTGGCAAAAGT 180 123 GGCATCCCTGTTTGGTACCGAACCAACCAGCAGCAACTCCCTGGCAAAACT 180 124 AAGCGTGCAACAACTGGAACTTAAGAGCACAACTGGAAACTCACTGGCAACACAC 124 AAGCGTGGCAACACTGGAATTTAAGAGCACAATTGAAACTCCCTGGCAAACTAACT

2 !		PECITION OF
g (S	2101 GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCGGTGCCCATGAGATTGCCCT 2160	Db
) [2101 GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCGGTGCCCATGAGATTTGCCCT 2160	Qy
, Ç	2041 ACATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTTCTCATTGACCGCGA 2100	Db
	2041 ACATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTTCTCATTGACCGCGA 2100	QY
ko Ko	981 CGGCCACCGGAACGGTCTTTGGTGGAGGAGTAGGAGCGATGATCGATC	Db
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ďū	961 AGCAGCTAGGCTGAGGCATAGCTGGAGCTGGAGCTGGTACGAGAGAGA	0ν
Qy	1001 AGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAQAAAGTTCGCG 1860	Db 43
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	741 AGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAG 1	OV
	1681 ACCAACTTCCGCTGAAGGCTGTGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG 1740	Db
Ç	1681 ACCAACTTCCGCTGAAGGCTGTGGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG 1740	Qy
BA	1621 CGATGTGTGGCGATGGTGTGTGGGCATGCTGGGTGAGCTTCTGACCGTTAAGCTGC 1680	Db
	1621 CGATGTGTGGCGATGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGC 1680	Qy
rg E	1561 CTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCG 1620	DЬ
	1561 CTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCG 1620	γQ
	1501 ACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCGCCCACGGCACGATGG 1560	Dβ
	1501 ACATCGAGAATCCGGAGGAACGCGCGACGTTTGTGGGTTCATTCCGCCACGGCACGATGG 1560	Qy
	1441 CGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCGAGGT 1500	DЪ
	1441 CGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCGAGGT 1500	Qy
	1381 ACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGG 1440	DЪ
	1381 ACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGG 1440	Qy
COI	1321 ATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGCTACACACATA 1380	Db
	1321 ATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATA 1380	Qy
3	1261 CTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGATCGTTCCTTCC	Db
ZO.	1261 CTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAAACAGATCGTTCCTTCC	Qγ
	1201 TCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGACGGTGTGTTG 1260	DЪ
SOS	1201 TCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTG 1260	Qy
KEN	1141 TGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGTTGCCCAGGTGGATA 1200	Db
AC:	1141 TGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGTTGCCCAGGTGGATA 1200	Qy
100	1081 GCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGATCTGCTGATTCTAT 1140	Db

RESULT 6 BD014868

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28-CCT-1999 DE 19951975.7

PI NICOLE DOUSH, BRIGITTE BAATE, JOERN KALINOVSKI, ALFRED PI PUEHLER, VETTYNA MECKEL,
PI ANKE WEISENBORN, WALTER PPEFFERLE
PC C12N15/09, C12N1/21, C12P13/08, C12P13/08///~~

PC C12N15/09, C12N1/21, C12P13/08, C12P13/08///~~

PC C12N15/09, C12N1/21, C12P13/08, C12P13/08///~~

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/mol_type="genomic DNA"
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.501 ACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTC	1441 CGGATAAGGATGCGGTGTTACTGTGGATACCGGCATGTGCAATGTV	1381 ACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTAT	1321 ATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGA 	1261 CTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGA 	1201 TCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGT 	1141 TGGGTACGGATTTCCCTTATTCTGATTTCCTTAAAGACAACGTTGC 	1081 GCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGA	1021 ATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGA 	961 TGAAGAATGCTCGCGCGCAGGTGTTGGAGTTTGGCGGAGAAGATTAAAT(901 CAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTTC	841 ATTCCAATTCCACTATTCTTCTGGCACTCCTGTGGTGTTCCCGGA	781 GTGTCTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGC 	721 GTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCAC 	661 AGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTG	601 CGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGG	541 CITGIGGICCIGGAAACACACCIGATICAGGGICTITAIGATIC	481 CGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGC	TI TO TO THE TOTAL CONTINUE TO THE TOTAL CON
CGCCACGGCACGATG	GTGTGGCATGCGAGGT	ATTTTGAACGAGCTGG	GAGACGTACACATA 	GATCGTTCCTTG GATCGTTCCTTCCTTG	GTGACCGGTGATGTTG 	GTTGCCCAGGTGGATA	GATCTGCTGATTCTAT	GAGGTCGGCATGTCTG	AAATCACCGATCGGGC	TTCTGCGGTGCGGGCG	GATCCTACTGAGGCTG	GCAGGTGACGGTACTT	ACCATGGCGGGTAAAG	TGCGAGATGGTGAATG	TGGTTCGACGTTCTTCC	TCGCATCGAAATGGTG TCGCATCGAAATGGTG	GCAGTATGTGCTGCTT - - - - - - - - - - - - - - - -	'CGAAATGAGGAAGCGG
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                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4 from Patent W00229020. AX404610
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Co. Ltd. And Kitasato University. Location/Qualifiers	FEATURES
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Satoshi Nakagawa, Kyowa Hakko K	AUTHORS TITLE JOURNAL
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Best Local Similarity
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AIHSPGLGSDMWIVGVCATGIGSVASALIMMTTILCHRARGKMWFRMPIFTWMIFVVS
VLALLIFPLLLAAALGYLYDRKLGGHLYDPANGGSLLWQHLFWFFGHPEVVLLLPFF
GIVSEILPVFSRKPMFGTVGLLFATLSIGALSMAVWAHHMFVTGAVLLDFFSFWTFLI
SVPTGVKFFNWVGTMWGGHTTWETPMIWSVGFMATFLEGGLTGIMLASPPLDFHLADS
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/gene="Cg12523"
/EC_number="1.9.3.1"
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GLLRRSKRLVCFDCDSTLITGEVIEMLAAHAGKEAEVAAVTERAMRGELDFEESLRER
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                                                                                                                                                                                                                                                                                                                                   /product-"Ribonucleotide reductase beta subunit"
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DPLKRKIASVILESFLFYSGFYLPMYWSSHSKLTNTADVIRLIIRDEAVHGYYIGYKY
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/gene="Cgl2525"
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9701. .10009
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HWVGNMGMPRRYADYLDSDGFTIYNQISTVFSFLLGLSVIPFIWNVFKSWRYGELVTV
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/db_xref="GI:21325294"
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11555. .12043
/gene="Cg12526"
/note="PF00210:Ferritin
                                                                                                                                                                                                                                                                                                        QKAVAKETPERQEELKEYTFDLLYDLYDNETQYSEDLYDDLGWTEDYKRFLRYNANKA
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/gene="Cgl2524"
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                                                                                                                                                                                                                                                                              _NNLGYEGLFPADETKVSPNILSALSPNADENHDFFSGSGSSYVIGKAENTEDDDWDF
100.0%; Score 2160; 100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115581 TTAGAGGCGATTCTGTGAGGTCACTTTTTGTGGGGGTCGGGGTCTAAATTTGGCCAGTTTT 115522
114561 ATGCGCTGGGTAGGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCATGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115041 CTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115161 TCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGG
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                                    1021 ATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCATGTCTG 1080
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                                                                                                                                                                901 CAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCG
                                                                                                                                                                                                                                                             841 ATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTG
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                                                                                                                                                                                                                                                                                                                                                                       GTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCACCATGGCGGGTAAAG 114802
                                                                                                                                                                                                                                                                                                                                                                                                           GTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCACCATGGCGGGTAAAG
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                                                                                                                                                                                                                       ATTCCAATTTCTTCTTCTGGCACTCCTGTGGTGTTCCCGGGATCCTACTGAGGCTG
                                                                                                                                                                                                                                                                                                                                     GTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATG 114862
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                                                                          TGAAGAATGCTCGCGCACGCTGTTGGAGTTGGCGGAAGATTAAATCACCGATCGGGC
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                       2101 GCGCTTAACTGCCAACATTTCCAAGATGGCAGCTCACGCCGGTGCCCCATGAGATTGCCCT 2160
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                   ACCAACTTCCGCTGAAGGCTGTGGTGTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG 1740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corynebacterium glutamicum genes encoding proteins involved
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KVREQLAEALAYPGPVLIDIVTDPNALSIPPTITWEQVMGFSKAATRTVFGGGVGAMI
DLARSNIRNIPTP
                                                                             PYSDFLPKDNVAQVDINGAHIGRRTTVKYPVTGDVAATIENILPHVKEKTDRSFLDRM
LKAHERKLSSVVETYTHNVEKHVPIHPEYVASILNELADKDAVETVDTGMCNVWHARY
IENPEGTRDFYGSFRHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVK
                                                                                                                                                                                                                                                                                                                             /organism="Corynebacterium
/mol_type="genomic DNA"
/db_xref="taxon:1718"
                                                                                                                                                                                                                                                                                               /note="RXN00635"
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1187 TGCCCAGGTGGAPATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGT 1246	7 7	1067 GGTCGGCATGTCTGGCCTGGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGA	y 1007 ATCACCGATCGGGCATGCGCTGGGTGAGCAGTACATCCAGCATGAGAATCCGTTTGA 1066	y 947 CTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAA 1006 	y 887 TCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTT 946	y 827 AGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGA 886	y 767 CATGGCGGGTAAAGGTGTGCGGTGGTAATTCCTGGTGATATCGCTAAGGAAGACGC 826 [[[]]]	y 707 CGAGATGGTGAATGGTGGTGAGCAGGTGAACGCATTTTGCATCACGCGATTCAGTCCAC 766	y 647 TICGACGITCTTCCAGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTG 706	y 587 GCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGG 646	y 527 AGTATGTGCTTCTTGTGGTCCTGGAAACACACACATTCAGGGTCTTTATGATTC 586	y 467 AAATGAGGAAGCGGCGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGC 526	407 CAGCCTTAATCCGATCGTGGATGCTGTCGGCCAATCAGATATTGAGTGGGTGCACGTTCG 466	y 347 ACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGTGGGTG	y 287 AAGTTAGGCAACACAATAGCCATAACGTTGAGGAGTTCAGATGGCACACACGCTACGCAGA 346	y 227 CTGGCAGGCGGAGCGAACAACTGGAATTTAAGAGCACAATTGAAGTCGCACC 286	Query Match 86.1%; Score 1860; DB 6; Length 1860; Best Local Similarity 100.0%; Pred. No. 0; Matches 1860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochlai,K., Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A. TITLE Novel polynucleotides JOURNAL Patent: EP 1108790-A 2873 20-JUN-2001; KYOWA HAKKO KOGYO CO., LTD. (JP)	Z		1727 by 1250 cm. 1250 cm.	Qy 2027 TCTGGCCCGTTCGAACATAAGGAATATTCCTACTCCATGATGATTGAT	Qy 1967 GGGATTCAGCAAGGCGGCCACCCGAACCGTCTTTGGTGGAGGAGTAGGAGCGATGATCGA 2026	1907 1681	2y 1847 GAAGAAAGTTCGCGAGCAGCTAGCTGAGCATATCCTGGACCTGTACTGATCGA 1906	1787 1561	1501	16 14	1607 C 1381 C	Qy 1547 CCACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAA 1606	QY 1487 GTGGCATGCGAGGTACATCGAGAAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCG 1546	Qy 1427 TTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGT 1486	Qy 1367 GACGTACACACACACAGCAGCAGCAGCAGTGCCCTGAATACGTTGCCTCTAT 1426 [130/ TOGTTLOCTTGATICGGATGCTICAAGGCACAGGACGTAAGTTGAGCTIGGGTGGTAGA 	1021

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                         GAGTTGGCGGAGAAGATTAAATCACCGATCGGGCATGCGCTGGGTGGTAAGCACTACATC
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                                               TICCTICCTAAAGACAACGTTGCCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGT 1226
                                                                       GATGCGTCCAATGAGGCGGATCTGCTGATTCTATTGGGTACGGATTTCCCCTTATTCTGAT 1166
                                                                                                                                                                    GAGTTGGCGGAGAAGATTAAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATC
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 ACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCT 1286
                                                                                                                      CAGCATGAGAATCCGTTTGAGGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTG
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/mol_type="genomic DNA"
/db_xref="taxon:1718"
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                       JOURNAL
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Novel polynucleotide
Patent: JP 2002191370-A 2873 09-JUL-2002;
KYOWA HAKKO KOGYO CO LTD
OS COrynebacterium glutamicum
                                     1 (bases 1 to 1737)
Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,A.
                                                                                            unidentified
                                                                                                                Novel polynucleotide.
BD165074
BD165074.1 GI:27870886
JP 2002191370-A/2873.
                                                                                unclassified
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DNA

linear

PAT 17-JAN-2003

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1681 GGAGTAGGAGCGATGATCGATCTGGCCCGTTCGAACATAAGGAATATTCCTACTCCA 1737
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                                                                              ### ATCACGTGGGAACAGGTCATGGGATTCAGCAAGGCGGCCACCCGAACCGTCTTTGGTGGA
                                                                                                                                                                                        CCTGGACCTGTACTGATCGATATCGTCACGGATCCTAATGCGCTGTCGATCCCACCAACC
                                                                                                                                                                                                                                                                            TTTGGTACTGACCATGAGGAAGTGAATTTCGCAGAGATTGCGGCGGCTGCCGGTATCAAA
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                                                                                                                                                                CCTGGACCTGTACTGATCGATATCGTCACGGATCCTAATGCGCTGTCGATCCCACCAACC
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PC C12P19/16
PC C12P19/16
G01N33/566,
PC G01N33/566,
PC C12N15/0
PC C12N15/0
PC C12N5/0
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                                   ACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAAC
                                                                                                                                                                                                                                                                                                            CATCACGCGATTCAGTCCACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGT
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                                                                                             ACTCCTGTGGGGTTCCCGGATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAAC
                                                                                                                                                       GATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP 2002191370-A/2873
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/mol_type="genomic DNA"
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 Mismatches

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GGAGTAGGAGCGATGATCGATCTGGCCCCGTTCGAACATAAGGAATATTCCTACTCCA 2063
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                                                                                                                 ATCACGTGGGAACAGGTCATGGGATTCAGCAAGGCGGCCACCCGAACCGTCTTTGGTGGA 2006
                                                                                                                                                                              CCTGGACCTGTACTGATCGATATCGTCACGGATCCTAATGCGCTGTCGATCCCACCAACC 1620
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                                     1503 ATCGAGAATCCGGAGGGAACGCGCGGCGACTTTGTGGGTTCATTCCGCCACGGCACGATGGCT 1562
                                                                                                                                                                                                                                                  1323 CGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATAAC
                                                                                                                                                                                      1383 GTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCG 1442
                                                                                       301
                                                                                                                                                                                                                                                                                        944;
                                                                                                                                                                                                                                                                                                                                                      61 AACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCT
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AX064963
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BASF AKTIENGESELLSCHAFT (DE)
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                                                                                   GATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCGAGGTAC
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FSKAATRTVFGGGVGAMIDLARSNIRNIPTP"
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DAVFTYDTGMCNYWHARYIENPEGTRDFYGSFRHGTMANALPHAIGAQSYDRNRQVIA
MCGDGGLGMLLGELLTYKLHQLPLKAYVFNNSSLGMYKLEMLYEGQPEFGTDHEEYNF
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/protein_id="CAC25721.1"
/db_xref="G1:12542676"
/translation="GTDFPYSDFLPKDNVAQVDINGAHIGRRTTVKYPVTGDVAATIE
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2043 ATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT 2086
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                                                                   1 TGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC
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          Dunican,L.K., Stapelton,C., Burke,K., Moeckel,B. and Thierbach,G. Process for the fermentative preparation of 1-amino acids with amplification of the tkt gene Patent: WO 0168894-A 5 20-SEP-2001; Degussa AG (DE); National University of Ireland (IE)
                                                                                                                                                   Corynebacterium glutamicum Corynebacterium glutamicum
                                                                                                                                                                                                                      Sequence 5 from Patent WO0168894.
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         CGCCACGGCACGATGGCTAATGCGTTGCCTCATGC 1579
                                               GTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTC 840
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Search completed: October

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

COMMENT	TITLE	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BH010685 LOCUS DEFINITION
Contact: W. Richard McComble Lita Anneaberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8844 Fax: 516 367 8874 Email: mccomble@cshl.org	V. Bell,M., Cunnius,D.M., King,L., Kirchoff,K., Kuit,K., Miller,B., Nascimento,L., Preston,R., Rodriguez,S., Santos,L., Shah,R., Vil,M.D., Zutavern,T., Bal,H., Dedhia,N. and McCombie,W.R. Whole Genome Shotgun Reads from Brassica oleracea Unpublished	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 601) Katari, M., O'Shaughnessy, A., Palmer, L., Bahret, A., Baker, J., Balija	genomic survey sequence. BH010685.1 GI:13956880 GSS. Brassica oleracea Brassica oleracea	BH010685 601 bp DNA linear GSS 04-MAY-2001 ep67h04.gl TO1000 Brassica oleracea genomic clone ep67h04 5',

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is from an A. gambiae BAC library provided by F.H Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (16.FEB-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-FEB-2000) BBMI, Institut Pasteur, Roux, Paris 75015, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poth, C.W., Brey, P.T., Ke, Z., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles gambiae (African malaria mosquito)
Anopheles gambiae

    Web : www.genoscope.cns.fr)

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GAGTTGGCGGAGAAGATTAAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATC 1046
                                                                                                                                                                     GACGTGGCGCTCAAGGCCGCGCGCGGNAAGGAGCCAACACCACACTGGTATCACGCGCCGC
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                                                                                                     AG-CCGGTGGTGACGCCAGCCGAGGAGGAGCTGAAAAAAGCTGGCGCASTGTCTGCGTTAC
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                                                                  GCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTG
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/note="end : T7"
277 c 261 g 1
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/clone="25I14"
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/strain="PEST"
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52.7%;
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Pred. No. 8.7e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library J. Bacteriol., (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence. B2571467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      msh2_1902.y2 msh Pseudomonas aeruginosa genomic clone msh2_1902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Washington Box 352145, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M. Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BZ571467.1 GI:27206528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: craymond@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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CGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCGCGATGT
                                                             CCTAGCACGGGCAAGCGCCTGCACCTTCACCAGCA-TGGTCCCCGGCACCATGGCCACGG
                                                                                                   AGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCGCCACGGCACGATGGCTAATG
                                                                                                                                         AGGACGCCCTGTTCACCNNCGACGTCGGCTCGGCGATGGTCTGGCTGTTGCGTCACAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATTTCCTTCCTAAAGACAACGTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGA 1223
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358 c
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/clone="msh2_1902"
/clone_lib="msh"
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/mol_type="genomic DNA"
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Pred. No. 9.4e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (sheep)
Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
CD288304
CD288304.1 GI:31086347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Thomas E. Spencer
Center for Animal Biotechnology and Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Gaprinae; Ovis.

1 (bases 1 to 487)
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3_P8.abd POE14_(Day_14_pregnant_ovine_endometrium) Ovis aries cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 9798454896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Animal Science Dept.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTGGTGATGCCGCCGAAGATCGAGT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAGAGATTG 1806
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  Conservative
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                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                            tspencer@ansc.tamu.edu
                                                                                         /tissue_type="endometrium"
/tissue_type="endometrium"
/dev_stage="Day 14 pregnant"
/clone_lib="POE14_(Day_14_pregnant_ovine_endometrium)"
/note="Organ: uterus; Vector: TriplEx2; Site_1: EcoR1;
/note="Organ: uterus; Vector: TriplEx2; Site_1: EcoR1;
Site_2: XhoI; Non-normalized library, Sequenced 5' with
Triplex2 primer (CTCCGAGATCTGGACGAGC). Library constructed
by Clontech with total RNA extracted using the Trizol
by Clontech with total RNA extracted using the Trizol
by Clontech with total RNA extracted using the Trizol
                                                                                                                                                                                                                                                                                                                                                                /organism="Ovis aries"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9940"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                   4.98;
  0
                Score 105.8; DB 1
Pred. No. 4.3e-19;
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  Mismatches 177;
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                                         DB 14;
                                         Length 487;
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                      Best Loc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                               Roux, Paris 75015, France This clone is from an A. gambiae BAC library provided by Collins and sequenced by Genoscope in collaboration with Laboratory of Biochem. and Biol. Molec. of Insects, Insti
                                                                                                                                                                                                                                                                                                                                     Submitted (16-FEB-2000) BBMI, Institut Pasteur, Roux, Paris 75015, France
                                                                                                                                                                                                                                                                                                                                                                                       Roth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS01FEV 731 bp DNA linear GSS 01-JUN-200 Anopheles gambiae GSS T7 end of clone 04F15 of NotreDame1 library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
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AL141752.1
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                                                                                                                                                                                                                                                                                                                                                                                                                     Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACGIGGCGTTAAAACCTGCGCCAGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCCATTTTG 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTT 686
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                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 731)
Ch.C.W., Brey.P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAGGTGTTTGGCCATCGCTAGCCAT 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 731)
                                                                                                       157
                      Conservative
                                                                                                 /clone_lib="NotreDame1"
/note="end : T7"
222 c 215 g 1
                                                                                                                                                  /strain="PEST"
/db_xref="taxon:7165"
/clone="04F15"
                                                                                                                                                                                                     /mol_type="genomic DNA"
                                                                                                                                                                                                                     /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:6999870
                                  4.9%;
               6;
                 Score 104.8; DB 29;
Pred. No. 1e-18;
5; Mismatches 270;
                                                                                                                                                                                                                                                                                and Biol. Molec. of Insects, Institut
                                                                                                   127
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                                                Length
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AUTHORS
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Direct Submission
Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue d
Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by
Collins and sequenced by Genoscope in collaboration with
                                                                                  - Web : www.genoscope.cns.fr)
2 (bases 1 to 375)
Roth,C.W., Brey,P.T., Ke,Z. and Collins,F
                                                                                                                                                                                                                                                                                                                                        CNS0713Y
375 bp DNA linear GSS 03-OCT-2001 Anopheles gambiae GSS SP6 end of clone 32N20 of library NotreDame1 from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
AL611872
                                                                                                                                    Submitted (01-OCT-2001) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                         Direct Submission
                                                                                                                                                                                           Genoscope
                                                                                                                                                                                                                        Anopheles.
                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                       Anopheles gambiae
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                                                                                                                                                                                                                                                                                       Anopheles gambiae (African malaria mosquito)
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Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                          GI:15963295
                                                                                                                                      National de Sequencage
segref@qenoscope.cns.fr
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                                                      Dr
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725 1046 665 986 606 806

429 746 370 686 626 251 566 191

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RESULT 7
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                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1696 AGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGGAGATGCTCGTGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 TCCCGCCGCAGATC 1
                                                                                                                               J. Bacteriol., (2002) In Contact: Chris K. Raymond
                                                                                                                                               Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                            msh2_1917.x1 msh Pseudomonas
Email: craymond@u.washington.eduClass: shotgun.
                                                                       University of Washington Box 352145, Seattle, WA
                                                                                                                                                                                                           Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.
Burns,J.L., Kaul,R. and Olsen,M.V.
                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                     BZ571498.1 GI:27206559
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                                                                                                                Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence.
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Similarity 54.3%;
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/note="end : SP6"
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/strain="PEST"
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                                                                     Seattle, WA 98105-2145,
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                                                                                 Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
                                                                                                                        Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                       Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamilds; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 538)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST274506 tomato seed, TAMU Lycopersicon esculentum cDNA clone
                                                                                                                                                                                                                                   ,S.D. and Giovannoni,J. Generation of ESTs from tomato seed tissue
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW036130.1 GI:5894809
EST.
                                                                                                                                                                                       Contact: CUGI
                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cLEE1G11 similar to pyruvate oxidase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW036130
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/note="Environmental isolate. Whole genomic shotgun
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/clone="msh2_1917"
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/strain="MSH"
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/organism="Lycopersicon
/mol_type="mRNA"
                                           1. .538
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                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 100; DB 29;
Pred. No. 2.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aeruginosa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                         Holt, I.E.
                                                                                                                                                                                                                                                                                                    Bowman
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RESULT 9
BZ559326
LOCUS
FEATURES
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                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 GCGCCAGAAGG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      765 ACCATGGCGGGTAAAAGGTGTGTCGGTGATTCCTGGTGATATCGCTAAGGAAGAC 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      585 TCGCATCGAAATGGTGCGAAGGTGTTGGCCCATCGCCTAGCCATATTCCGAGTGCCCAGATT 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 GCGGTCTGCGCCGGATCGTGCGGCCCCGGCAACCTGCACTTAATCAACGGCCTGTTCGAT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 CCCCACGAATAAGTGGCGGCCTTTGCCGCTGGCGCTGAAGCACAACTTAGCGTAGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 TGCGAGCTGGTTTCCAGCCCGGAGCAGATCCCACAAGTACTGGCGATTGCCATGCGCAAA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            705 TGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 TGCCACCGCAATCACGTTCCGGTACTGGCGATTGCCGCTCATATTCCCTCCAGCGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 GCAGTATGTGCTTCTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 CGAAATGAGGAAGCGGCGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTG
                                                                                                                                                                                                                             Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1037)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pacs2-164_1412.s1 pacs2-164 Pseudomonas aeruginosa genomic clone
pacs2-164_1412, genomic survey sequence.
                                                                         University of Washington
Box 352145, Seattle, WA
Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                      Class: shotgun
                                                                                                                                                                              Genome Center
                                                                                                                                                                                                          Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BZ559326.1 GI:27175469
                                               Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGGTGACGG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGGTGCTTAACCGTGGCGTTTCGGTTGTCGTGTTACCAGGCGACGTGGCGTTAAAACCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAGCGGCTATTTCCAGGAAACCCACCCACACAAGAGCTATTCCGCGAATGTAGTCACTAT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTAC 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="tomato seed, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; cLEE - Tomato Seed EST Library. Directionally cloned
cDNAs inserted into pBlueScript SK(-) at 5' end with
ECORI and 3' end with XhoI site."
a 154 c 156 g 119 t
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/dev_stage="quiescent seed"
/lab_host="XL1-Blue MRF'"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4081"
/clone="cLEE1G11"
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53.68;
                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas.
                                                                                                                           WA 98105-2145,
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Pred. No. 3.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1037 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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Dβ 20 Qγ Вb γg Вb

Дb

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                                                                KEYWORDS
                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                             BG627542/c
                                                                                                                                                                                                                                     RESULT 10
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                                                                                         VERSION
                                                                                                                                                                                             Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1063 TTGAGGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCGCGTGGATGCGTCCAATGAGG 1122
                                                                                                                                                                                                                                                                                                                                          1660 AGCTTCTGACCG 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1540 CATTCCGCCACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTG 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1480 GCAATGTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTT 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1420 CCTCTATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGT 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1360 TGGTAGAGACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCCTGAATACGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1300 AAACAGATCGTTCCTTCGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGG 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1240 ATCCGGTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAA 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1180 ACAACGTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 CCACCCTGATCCAGGTCGACCGCGATGGCAGCCACCTGGGCCGCCGCCCACCCCATCGATC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 GCCTGGTCCACGGCACCATGGCCAACGCCATGCCCCAGGCGCTGGGACTGAAGAAGGCCT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 TCAGCCTGCTCGACCAGCACGCCAGCGACGCCCTGTTCACCGCCGACGGCGTCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 TGGAAAAAGGAGGAG-----CAAGCCGGCAAGGGCTGATCCATCCGCAGCACCTGG
                                                                                                                                                                                                                                                                                                  611 ACCTGCTGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 GCGACACCCTCCTGCTCCGCCGCCCCGACTTCGCCTGGGCCCAGTTCTATCCGCAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 TAGAGGATCCCCTGACCGGTATGCTCGGGATCGAGTCCGGCTTCCACATGATGACCGAGT
                                                                                                                          cC-esflcLEL18A13a1 Tomato flower library from a mixture of developmental stages Lycopersicon esculentum cDNA clone cC-esflcLEL18A13a1, mRNA sequence.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                        Lycopersicon esculentum (tomato)
                                                                                       BG627542.1 GI:13679015
                                                                                                                                                                                         BG627542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGGCGTGGTCGGCGACGTGATCCCCCACCCTCGAGGCGCTCTTGCCATTGCTCGAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                    ATCGAAACCGCCAGGTGATCGCGATGTGTGGCGATGGTGGTTTTGGGCATGCTGCTTGGTG
                                                                                                                                                                                                                                                                                                                                                                                  ACCCCGAGCGCCAGGTGATCTCCGATCTCCGGCGACGGCCTGGCCATGCTGCTCGGCC
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/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="2-164"
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51.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 91.6; DB 29; Pred. No. 8.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                         274 bp
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                                                                                                                                                                                         mRNA
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                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                       EST 19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                610
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RESULT 11
BM534496/c
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                                                          REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               687 AAGGAATGCTCTGGTTACTGCGAG 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 CAACTTAGCGGAGAACTGGCGGTCTGCGCCGGATCGTGCGGCCCCGGCAACCTTGCACTTA 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 ATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAATCG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 ATTCCCTCCAGCGAAATTGGCAGCGGCTATTTCCAGGAAACCCACCACCACAAGAGCTATTC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 550)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
                                                                                                                                                                                                                                                          fw89h06.y1 Gong zebrafish ovary Danio rerio cDNA clone
IMAGE:5617763 5' similar to SW:POXB_ECOLI p07003 PYRUVATE
DEHYDROGENASE ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESTs from a tomato flower library Unpublished Contact: Rutger S. van der Hoeven
                                                                                                                                                Danio rerio
                                                                                                                                                                                                                                         BM534496
                                                                                                                                                                                                                                                                                                                                    BM534496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 274)
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                    Danio rerio (zebrafish)
                                                                                                                                                                                                                   BM534496.1 GI:18745505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTT 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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607 255 6683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Tomato flower library from a mixture of developmental stages" developmental stages" /note="Vector: pBK_CMV; Site_1: EcoRI; Site_2: xhoI; Flowers and flower buds were collected from greenhouse grown plants and used for library construction (cDEL).

a 74 c 87 g 59 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="developing flower buds and open flowers"
/dev_stage="4-8 week old plants"
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/clone="cC-esflcLEL18A13a1"
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                                                                                              196 CGTGAATGTAGTCGCTATTGCGAGCTGGTTTCCAGCCTGGAGCAGATCCCACAAGTACTG 137
                                                                                                                                                        687 AAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTG 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University Genome Sequencing Center St. Louis. Pl. contact Zhiyuan Gong for further information on this library CNAtional University of Singapore, Department of Biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished Other_ESTs: fw89h06.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 1.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                      ATTCCCTCCAGCGAAGTTGGCAGCGTCTATTTCCAGGAAACCCCACCACAAGAGTTATTG 197
                                                                                                                                                                                                                                                                                                                                           ATCAACGGCCTGTTTGATTCCCTAAGCAATCGCGTTCCGGTACTGGTGATTGCCGCTCAT 257
                                                                                                                                                                                                                                                                                                                                                                                                      ATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCAT 626
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/clone_lib="cong_zebrafish_ovary"
/clone_lib="cong_zebrafish ovary"
/clone_lib="cong_zebrafish ovary"
/note="crgan: ovary (pooled); Vector: pBluescript SK:
/note="crgan: ovary (pooled); Vector: pBluescript SK:
/note="cong_note-broad bluescript SK | Poly A + RNA was isolatd from
the ovaries of 2 female adult zebrafish (4-5 month old).

CDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University protocol
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/sex="female"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                   643 TTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTT 702
                                                                                                                                                                                                                                                                                                          523 TGGCAGTATGTGCTGCTTCTTGTGGTCCTTGGAAACACACCTGATTCAGGGTCTTTATG 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Washington
Box 352145, Seattle, WA 98105-2145, USA
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J. Bacteriol., (2002) In press
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: craymond@u.washington.edu
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                                  ACGCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCC
                                                                          CCACCATGGCGGTAAAAGGTGTGTCGCGGTGGTAGTGATTCCCTGGTGATATCGCTAAGGAAG 822
                                                                                                                                                    TCTGCGAGCAGGTGCACAGCCCGGAACAGGCGCGCGCGGGTGGTGGCCCTGCCCAGG
                                                                                                                                                                                       ACTGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGT 762
                                                                                                                                                                                                                              TGGGCATGGAGTTTCCCCCAGGAGGTCGACTTCAAGGCGGTCTACGCCAGCTGCTCGGTGT 420
                                                                                                                                                                                                                                                                                                                                               ATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGA 642
                                                                                                                                                                                                                                                                                                                                                                                      TGACCGCCTGCGCCGGCTCNTGCGGACCGGGCAGCCTGCACTTCATCAACGGCGTCTACG
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/clone="pacs1-60_2172"
/clone_lib="pacs1-60"
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/mol_type="genomic DNA"
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                       461 CGTTCGAAATGAGGAAGCGGCGGCGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 TCAAGGCGCCCATCGCGCACACGTCGCGGACCAAGGACTTCGTCGAGTACGACAACCCCT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 TCTACGCCGGCTGCCAGGGCGCCCACGACCTGCTGGTGGCCCTCGCCGACCGCC 126
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                                                                                  492 CGGCGACACCCTCAACCATGTCACCGACGCCATCCATCGCAGCCAGATCCAGTGGGTACA
                                                                                                                               401 GGGTGACAGCCTTAATCCGATCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCA 460
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Spencer,D.H., Raymond,C.K., Smith,
Burns,J.L., Kaul,R. and Olsen,M.V.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: craymond@u.washington.edu
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/mol_type="genomic DNA"
/strain="MSH"
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/clone="msh2_1969"
/clone_ib="msh"
/note="Environmental isolate. Whole genomic shotgun
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RESULT 14
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                       1784 GGAAGTGAATTTCGCAGAGATTGCGGCGGCTGCGGGTATCA 1824
                                                                                                                     1724 GGGCATGGTGAAGTTGGAGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGA 178:
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                                                                                                                                                              136 CCTCTCAGTAGTGCAGATGAAACTGCCAGTGAAAATTGTCGTCTTTAACAACAGCGTGCT
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Class: sheared ends.
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From Wash. U contig 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Survey sequencing of Arabidopsis thaliana BAC F26J2J
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CGACACAAACTTTGCCCGCATTGCCGAAGCGTGCGGCATTA 296
                                                                              (bases 1 to 299)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medical Center Drive, Rockville, 301-838-3523
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  73
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pHOS2; Site_1: BstXI; 2-3 kb sheared BAC
DNA inserted into pHOS2 using BstXI linkers"
66 c 84 g 76 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="AUIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3702"
/clone="AUILB19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                57.98;
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                            Score 72.2; DB 28;
Pred. No. 1.7e-09;
0; Mismatches 93;
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Locus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                               1909 TC 1910
                                                                                                                                                                                                                                  1789 TGAATTTCGCAGAGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGA 1848
                                                                                                                                                                                                                                                                                                                         1729 TGGTGAAGTTGGAGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAG 1788
                                                                                                                                                                                                                                                                                                                                                                                                                     1669 CCGTTAAGCTGCACCAACTTCCGCTGAAGGCTGTGTGTTTAACAACAGTTCTTTGGGCA 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1022 GACAAGTTTGGTCAATTTCTGGGGATGGAGCTTGGGCGATGGTGATGCCTGATATTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1609 GCCAGGTGATCGCGATGTGGCGATGGTGGTTTGGGCATGCTGGTGAGGCTTCTGA 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1082 ATGCTACGATGGGCTATGCTTTGCCGGCAGCAATTGGGGCCAAGTCTCAATATCCAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1549 ACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACC 1608
                                                                                                                                   1849 AGAAAGTTCGCGAGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGATA 1908
722 TC 721
                                                                                         782 CAGAACTGAAAGAGCCTTTGCAAAAGCGAAAGAACTGATCGACCAGTTGTCATTAATG 723
                                                                                                                                                                                   842 CAAATTTTGGAGCTTCGGCAGCAGCTTTGGGTGCAGTAGGGTTTGATGTCAATAACTTGT 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subsp. ci
BH770875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis subsp. cremoris Lactococcus lactis subsp. cremoris
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LLMGtag610 MG1363 Random Sequence Tag Library Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 1834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 33 1 34 65 25 16 Fax: 33 1 34 65 25 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetique Microbienne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Sorokin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments, (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH770875.1 GI:20373832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         best homologue in strain IL1403 is poxL (89%)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: sorokine@jouy.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus
                                                                                                                                                                                                                                                                                 TTATTGAAGCAGAACAAGATGATGCCAAACAACCACACTCTGGTATTGATTTGATTGGAG
                                                                                                                                                                                                                                                                                                                                                                           CTCAGGTCAAATACCATTTACCAATCATTAATGTTGTTTTAACTAATAAGAGCCTAGGCT 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 1862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cremoris genomic, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site_1: Smal; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."
a 384 c 282 g 649 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="MG1363"
/db_xref="taxon:1359"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Lactococcus lactis subsp. cremoris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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49.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1862 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1862;
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Search completed: October 3, 2003, 18:49:55 Job time : 4101 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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110:
110:
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2160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA: *
: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	a	o	Result No.
14 15 16	10 112 113	0 w 4 N 0 L (0)0	1t
344.8 324.4 305.2	875 875 523 522.6	2160 2160 2160 2160 2160 2160 1737 875 875	Score 2160
		100.0 100.0 100.0 100.0 100.0 80.4 40.5	Query Match
1719 1422 1719	875 875 9025608 1740	2160 2160 2160 2160 3248 3309400 1737 875 875	Query Match Length DB
9 10	14 14 14	12 14 10 10 10 10	0;
US-09-815-242-9898 US-09-965-825-12 US-09-815-242-6012	US-10-143-856-5 US-10-078-167-6 US-10-156-761-1 US-10-156-761-2067	US-10-336-049-4 US-10-143-856-3 US-10-0748-457-4 US-09-965-825-4 US-09-738-626-1 US-09-738-626-2873 US-09-738-626-2873 US-09-738-749-6	US-09-965-825-1)
Sequence 9898, Ap Sequence 12, Appl Sequence 6012, Ap	Sequence 5, Appli Sequence 6, Appli Sequence 1, Appli Sequence 2067, Ap	Sequence 4, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 2873, Ap Sequence 3, Appli Sequence 6, Appli	Description Sequence 1, Appli

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2.4	ر 4	2.4	2.5	2.5	2.6	2.6	2.6	2.8	2.9	3.1	3.2	3.2	3.2	3.2	3.6	3.7	3.7	4.6	5.7	6.4	6.5	6 5	7.1	7.2	9.5	9.6	9.7	14.1
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US-10-307-138-9	115-00-974-300-493	US-09-974-300-481	US-09-767-878-1	US-10-156-761-2720	US-10-329-960-1	US-09-732-618-42	US-09-887-194A-35	JS-09-815-242-9527	US-09-815-242-6310	US-09-815-242-9937	US-10-096-595B-13	US-10-096-595B-11	US-10-096-571-13	US-10-096-571-11	US-09-738-626-2854	US-09-815-242-1850	US-09-738-626-1	US-09-815-242-4044	US-09-974-300-480	US-08-781-986A-138	US-09-815-242-8845	JS-09-815-242-4766	US-10-096-571-8	us-10-096-571-7	US-10-156-761-943	US-10-156-761-1	US-09-738-626-2872	T-1)C-060-01-00
Sequence 9, Appli		Sequence 481, App	Sequence 1, Appli	Sequence 2720, Ap	Sequence 1, Appli	Sequence 42, Appl	Sequence 35, Appl	Sequence 9527, Ap	Sequence 6310, Ap	Sequence 9937, Ap	Sequence 13, Appl	11,	Sequence 13, Appl	11,	Sequence 2854, Ap		Sequence 1, Appli	Sequence 4044, Ap		. Sequence 138, App	Sequence 8845, Ap	Sequence 4766, Ap	Sequence 8, Appli	Sequence 7, Appli	Sequence 943, App	Sequence 1, Appli	Sequence 2872, Ap	sequence 1, Appli

ALIGNMENTS

RESULT 1 US-09-965-825-1

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; OTHER INFORMATION: US-09-965-825-1
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09965825 Patent No. US20020150999A1 GENERAL INFORMATION:
                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DUSCH, Nicole
APPLICANT: THOMAS, Hermann
APPLICANT: THERBACH, Georg
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACTIVE OF INVENTION: CORVNEFORM BACTERIA
FILE REFERENCE: 213540SOX
CURRENT APPLICATION NUMBER: US/09/965,825
CURRENT FILING DATE: 2001-10-01
CURRENT FILING DATE: 2001-10-01
    Matches 2160;
                                                                                                                                    NAME/KEY: -35_signal LOCATION: (227)..(232) OTHER INFORMATION: NAME/KEY: -10_signal LOCATION: (256)..(261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: DE 10048604.5
PRIOR FILING DATE: 2000-09-30
PRIOR APPLICATION NUMBER: DE 10117085.8
                                                                                                                                                                                                                                                           LOCATION: (327)..(2063)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Corynebacterium glutamicum
100.0%; Score 2160; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
                                            DB 10; Length 2160;
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2101 GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCGGTGCCCATGAGATTGCCCT 2160	2041 ACATAAGGAATATTCCTACTCCATGATGATGATACACCTGCTGCTGTTCTCATTGACCGCGA 2100	1981 CGGCCACCCGAACCGTCTTTGGTGGAGGAGTAGGAGCGATGATCGATC	1921 CTAATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCATGGGATTCAGCAAGG 1980	61 AGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGATATCGTCACGGATC	1801 AGATTGCGGCGGCTGCGGGTATCAAATCGGTACGATCACCGATCCGAAGAAGATTCGCG 1860 	1741 AGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAG 1800	1681 ACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG 1740	1621 CGATGTGTGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGC 1680	1561 CTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCG 1620	1501 ACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCGCCACGGCACGATGG 1560	1441 CGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGCCATGCGAGGT 1500	1381 ACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGG 1440	1321 ATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATA 1380	1261 CTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAACAGATCGTTCCTTCTTG 1320 	1 TCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTG 1	1141 TGGGTACGGATTTCCCTTATTCTGATTTCCTTAAGACAACGTTGCCCAGGTGGATA 1200 	

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LENGTH: 2160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 2160;
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fittle OF INVENTION: Process for the Preparation
TITLE OF INVENTION: the zwf Gene
FILE REFERENCE: 7601/80158
CURRENT APPLICATION NUMBER: US/10/336,049
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 37
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APPLICANT:
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LOCATION: (327)..(2
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Corynebacterium glutamicum FEATURE:
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Reth, Alexander
Thierbach, Georg
Kreutzer, Caroline
                                                                                                     CGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTT
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               CGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCC
                                              CTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTG
                                                                          CTTGTGGTCCTGGAAACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTG
                                                                                                                                    CGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTT
                                                                                                                                                                TCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGG
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CGATGTGTGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGC
                                                                                                                                  CTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCG
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                            ACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG 1740
                                                          CGATGTGTGGCGATGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGC
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LENGTH: 2160

TYPE: DNA
ORGANISM: Corynebacterium gl
FEATURE:
NAME/KEY: CDS
LOCATION: (327)...(2063)
OTHER INFORMATION: poxB
US-10-143-856-3
                                                                                                                                                                                                                                                             APPLICANT: BURKE, KEVIN
APPLICANT: BUNKE, KEVIN
APPLICANT: DUNICAN, L.K.
APPLICANT: MCGORMACK, ASHLING
APPLICANT: STAPLETON, CLIONA
APPLICANT: STAPLETON, CLIONA
APPLICANT: THIERBACH, GEORG
TITLE OF INVENTION: Process for the fermentative preparation of
TITLE OF INVENTION: With amplification of the tkt gene
FILE REFERENCE: MAS/021123/28432
CURRENT APPLICATION NUMBER: US/10/143,856
CURRENT APPLICATION NUMBER: 09/86,649
PRIOR APPLICATION NUMBER: 09/86,649
PRIOR FILING DATE: 17-03-2000
NUMBER OF SEQ ID NOS: 12
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                                                                                     Sequence 4, Application US/10078167 Publication No. US20030119154A1 GENERAL INFORMATION:
APPLICANT: Dunican, Rita
APPLICANT: McCormack, Ashling
APPLICANT: Stapleton, Cliona
APPLICANT: Burke, Kevin
APPLICANT: Mockel, Bettina
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GENERAL INFORMATION, Nicole
APPLICANT: DUSCH, Nicole
APPLICANT: THOMAS, Hermann
APPLICANT: THIERBACH, Georg
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACITILE OF INVENTION: CORYNEFORM BACTERIA
FILE REFERENCE: 21354USOX
                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 2160;
Best Local Similarity 100.0%; Pred. No. 0;
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LENGTH: 3248
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                                                                                                                                                                                                                                                                                                                                         Matches 2160;
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PRIOR FILING DATE: 2000-09-30
PRIOR APPLICATION NUMBER: DE 10117085.8
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2001-10-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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GGGCATCCCTGTTTGGTACCGAGTACCCACCCGGGCCTGAAACTCCCCTGGCAGGCGGCCG
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1321 ATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATA 1380	261 736	1201 TCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTG 1260	1141 TGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGTTGCCCAGGTGGATA 1200 	1081 GCCTGCTTAGGTTACGGCGCCTGGGTGGATGCGTCCAATGAGGCGGATCTGCTGATTCTAT 1140 	1021 ATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCATGTCTG 1080	961 TGAAGAATGCTCGCGCGCAGGTGTTGGAGTTTGGCGGAGAAAATTAAATCACCGATCGGGC 1020 	901 CAGCGCTGGAGGCGAFTAACAACGCTAAGTCTGTCACTTTGTTCTGCGGTGCGG	841 ATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTG 900	781 GTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTT 840 	721 GIGGIGAGCAGGGIGAACGCAITITGCAICACGCGAITCAGICCACCAIGGCGGGIAAAG 780 	661 AGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATG 720 	601 CGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCC 660 	541 CTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTG 600	481 CGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTT 540	421 TCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGG 480	361 CTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGTGGGTG	301 AATAGCCATAACGTTGAGGAGTTCAGATGGCACAGCTACGCAGAACAATTAATT
FILLE FOR INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18 PRIOR APPLICATION NUMBER: JP 99/377484 PRIOR FILING DATE: 1999-12-16	APPLICANT: TATEISHI, NAORO APPLICANT: SENOH, AKIHIRO APPLICANT: IKEDA, MASATO APPLICANT: OZAKI, AKIO	APPLICANT: ANDO, SEIKO APPLICANT: HAKYASHI, MIKIRO APPLICANT: OCHIAI, KEIKO APPLICANT: YOKOI, HARUHIKO	; PUDLICATION NO. US20020197605A1 ; GENERAL INFORMATION: ; APPLICANT: NARAGAWA, SATOSHI ; APPLICANT: MIZOGUCHI, HIROSHI	RESULT 6 US-09-738-626-1/c ; Sequence 1, Application US/09738626	QY 2101 GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCGGTGCCCATGAGATTTGCCCT 2160	Qy 2041 ACATAAGGAATATTCCTACTCCATGATGATGATACACCTGCTGTTCTCATTGACCGCGA 2100	QY 1981 CGGCCACCCGAACCGTCTTTGGTGGAGGAGTAGGAGCGATCGAT	1921 2396	1861 2336	1801 2276		Qy 1681 ACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG 1740	621 096	1561 2036	501 976	1916	1856

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; ORGANISM: Corynebacterium glutamicum
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SEQ ID NO 1
LENGTH: 3309400
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                   2778050 GTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTT 2777991
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                                                                                                              AGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTT 540
ATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGGATCCTACTGAGGCTG
                                                          GTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTT 840
                                                                                                                                                                                                                                                                                                CGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCC 660
                                                                                                                                                                                                                                                                                                                                                                                              CTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTT 277829:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGG 2778351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATG 2778111
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Qy	DЬ	Qy	Db	Qy	Дb	DЬ	Qy	Db	Qy	Db Qy	Db	Qy	Db	OV V	Db	Ωу	Db Qy	DЬ	Qy	ф	Qy	Db	дь	Qy	Дb	Qy	Db	γQ	Db	Дb
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CTAATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCATGGGATTCAGCAAGG	AGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGATATCGTCACGGATC	AGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGATATCGTCACGGATC	AGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAGAAGTTCGCG	AGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAGAAAGTTCGCG	AGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAG		ACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG	CATGTGTGGCGATGGTGGTTTGGGCATGCTGCTGAGCTTCTGACCGTTAAGCTGC	CGATGTGTGGCGATGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGC	CTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCG		ACATCGAGAATCCGGAGGGAACGCGCGCACTTTGTGGGTTCATTCCGCCACGGCACGATGG			### ACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGG		ATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATA		CTGCAACAATGGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGATCGTTCCTTCC	TCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTG		TGGGTACGGATITCCCTTATICTGATITCCTTCCTAAAGACAACGTTGCCCAGGTGGATA	GCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGATCTGCTGATTCTAT	GCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGATCTGCTGATTCTAT	ATGCGCTGGGTAGGAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCATGTCTG		TGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGC		CAGCCCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGGGGGAGGGGGGGG	
1980	2776911	1920	2776971	1860	1800 2777031	2777091	1740	2777151	1680	1620 2777211	2777271	1560	7 (1500	77	1440	1380 2777 4 51	2777511	20	2777571	1260	1200 2777631	2777691	40	2777751	1080	2777811	1020	2777871	2777931

Qy 567 ATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCAT 626	507	447 ATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGTTGCCAGCCGGTGCGGAATCG 5		327 ATGGCACACAGAGCAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGA 38	Query Match 80.4%; Score 1737; DB 10; Length 1737; Best Local Similarity 100.0%; Pred. No. 0; Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059 SOFTWARE: PatentIn ver. 3.0 SEO ID NO 2873	PRIOR FILING DATE: 1999-12-16 PRIOR APPLICATION NUMBER: JP 00/15 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: JP 00/28	FILE CURRI CURRI PRIOI	APPLICANT: SENOH, AKIHIRO APPLICANT: IKEDA, MASATO APPLICANT: OZAKI, MASATO TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES	APPLICANT: APPLICANT: APPLICANT:		RESULT 7 US-09-738-626-2873 ; Sequence 2873, Application US/09738626 ; Dublication No. US20020197605A1		2776790 ACATAAGGAATATTCCTACTCCATGATGATGACACGCGGTGCTCTTTAACTGCGCGA		Db 2776910 CTAATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCATGGGATTCAGCAAGG 2776851 Qy 1981 CGGCCACCCGAACCGTCTTTGGTGGAGGAGTAGGAGGGATGATCGATC
QY 1647 AUGCTGCTGGGTAGGCTTCTGACCGTTAGACGCCACAACTTCCGCTGAAGGCTGTGGTG 1706	1587 GCGCAAAGTGTTGATCGAAACCGCCAGGTGATCGCGATGTGTGGGGATGGTTTGGGC	QY 1527 GACTTTGTGGGTTCATTCCGCCACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGGT 1586	QY 1467 GATACCGGCATGTGCAATGTGGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGC 1526	QY 1407 CCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTG 1466	Qy 1347 AAGTTGAGCTCGGTGGTAGAGACGTACACACATAACGTCGAGAAGCATGTGCCTATTCAC 1406	Qy 1287 CATGTGAAGGAAAAAACAGATCGTTCCTTGATCGGATGCTCAAGGCACACGAGCGT 1346	Qy 1227 ACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCT 1286	Qy 1167 TTCCTTCCTAAAGACAACGTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGT 1226	Qy 1107 GATGCGTCCAATGAGGCGGATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGAT 1166	Qy 1047 CAGCATGAGAATCCGTTTGAGGTCGGCATGTTGGCTTGGTTACGGCGCCTGCGTG 1106 	Qy 987 GAGTTGGCGGAGAAGATTAAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACAIC 1046	Qy 927 GCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTG 986	Qy 867 ACTCCTGTGGGGTTCCCGGATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAAC 926	Qy 807 GATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCCACTATTTCTTCTGGC 866	QY 747 CATCACGCGATTCAGTCCACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGT 806	QY 687 AAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGTGAGCAGGTGAACGCATTTTG 746	

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CURRENT APPLICATION NUMBER: US/09/965,825
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: DE 10048604.5
PRIOR FILING DATE: 2000-09-30
PRIOR APPLICATION NUMBER: DE 10117085.8
PRIOR ETLING DATE: 2001-04-06
PRIOR ETLING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DUSCH, Nicole
APPLICANT: THOMAS, Hermann
APPLICANT: THOMAS, Hermann
APPLICANT: THIERBACH, Georg
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACID
TITLE OF INVENTION: CORYNEFORM BACTERIA
FILE REFERENCE: 21354USOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 40.5%; Score 875; DB 10; Length 87 Local Similarity 100.0%; Pred. No. 1.5e-277; National States 10; Indels
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       1005 AAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 1064
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                                                                                                                                                                                                                                                            825 GCAGGTGACGTACTTATTCCAATTCCACTATTCTTCTGGGCACTCCTGTGGTGTTCCCG
                                                                                                                                         181 GATCCTACTGAGGCTGCAGGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTG
                                                                                                                                                                                                                                                                                                                                                      765 ACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC
                                                                                          945 TTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAAGTTTGGCGGAGAAGATT 1004
                                                                                                                                                                                     885 GATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    705 TGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATT
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                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10336049
Publication No. US20030175911A1
                                                                                                                                    Best Local Similarity
Matches 875; Conserva
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/336,049
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mockel, Bettina TITLE OF INVENTION: Process for the Preparation of L-Amino Acids with Amplificatio TITLE OF INVENTION: the zwf Gene FILE REFERENCE: 7601/80158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hans, Stephan
APPLICANT: Bathe, Brigitte
APPLICANT: Reth, Alexander
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APPLICANT:
                                                                                                                                                                                                                                        LENGTH: 875
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1425 ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAAT 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1365 GAGACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT 1424
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                                                                           705 TGCGAGATGGTGAATGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            841 CGCCACGGCACGATGGCCTAATGCGTTGCCTCATGC 875
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Kreutzer, Caroline
                                                                                                                                      Conservative
                                                                                                                                 40.5%; Score 875; DB 12; Length 875; 100.0%; Pred. No. 1.5e-277; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                       Sequence 5, Application US/10143856 Publication No. US20030109014A1 GENERAL INFORMATION:
APPLICANT: BURKE, KEVIN
APPLICANT: DUNICAN, L.K.
APPLICANT: MCCORMACK, ASHLING
APPLICANT: MCCORMACK, ASHLING
APPLICANT: STAPLETON, CLIONA
APPLICANT: THIERBACH, GEORG
TITLE OF INVENTION: Process for the fermentative preparation of
TITLE OF INVENTION: with amplification of the tkt gene
FILE REFERENCE: MAS/021123/282432
CURRENT APPLICATION NUMBER: US/10/143,856
CURRENT APPLICATION NUMBER: 2002-05-14
PRIOR APPLICATION NUMBER: 09/986,649
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; SEQ ID NO 5
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium g
US-10-143-856-5
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841 CGCCACGCCACGATGCCTAATGCGTTGCCTCATGC

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-10-078-167-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 6
LENGTH: 875
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APPL:CANT: McCormack, Ashling
APPLICANT: Stapleton, Cliona
APPLICANT: Burke, Kevin
APPLICANT: Mockel, Bettina
TITLE OF INVENTION: Process for the preparation of L-amino acids using
TITLE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
FILE REFERENCE: 99029 BT-US-B
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CURRENT FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATCACCGATCGGGCATGCGCTGGGTGATAGCAGTACATCCAGCATGAGAATCCGTTT 1064
GAGACGTACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT 1424
                                   GATCGTTCCTTCATCGGATCCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA 660
                                                          GATCGTTCCTTGCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTA 1364
                                                                                                                 GTGACCGGTGATGTTGCCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAAACA 1304
                                                                                                                                                                                                                    GTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCG 1244
                                                                                                                                                                                                                                                                             GATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTACTAAAGACAAC 480
                                                                                                                                                                                                                                                                                                  GATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTACTTCCTAAAGACAAC 1184
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                                                                                                                                                                                               GTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCCGGAGAAGATT
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c,
US-10-156-761-1
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US-10-156-761-1/c
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APPLICANT:
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 9025608
TYPE: DNA
                                                                                                                                                                                                                       2532215 CAACGGCCTGTACGACGCCCACCGCTCCATGGCGCCCGGTCCTCGCCCTCGCCTCGCACAT 2532156
                                                                                                                                       2532275 GATCACCGGCAAGCTCGCCGCCTGCGCCGGCTCCTGCGGCCCCGGGAACCTCCACCTCAT
                                                                                                                                                                                                                                                                                                                                                                                    2532455 ACAGAACGTCGCCGAGCAGTTTGTCGACATCCTCGTCCGCGCGGGGCGTCAATCGCCTGTA 2532396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                   629 TCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTTAA 688
                                                                                                                                                                                                                                                                                                                                           392 TGGTTTGGTGGGTGACAGCCTTAATCCGATCGTGGATGCTGTCCGCC---AATCAGATAT 448
                                                                                                                                                                                                                                                                                                                                                                                                                           332 ACACAGCTACGCAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGAATTTA 391
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                                                                                              TCAGGGTCTTATGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATAT
                                                                                                                                                               TGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGTTTTGCAGCCGGTGCGGAATCGTT 508
                                                                                                                                                                                                                                                                                                    CGGGGTGGTGACAGTCTCAACCCGGTCGTCGACGCCATTCGGCGCCAACTCCGCCAT
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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Pred. No. 5.2e-159;
0; Mismatches 720;
Indels
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            GTTCAACAACTCCTTCAGCATGCTCGAGTTGGAGATGCTGGTGGCCGGGCTGCCCTC 2531022
                                                  GTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGGAGAGTGCTCGTĞGAGGGACAGCCAGA
                                                                                                           CATGCTGATGGGCGACTTCCTCACCCTCGTCCAGTACGACCTGCCGGTGAAGGTCGTACT
                                                                                                                                          CATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGCACCAACTTCCGCTGAAGGCTGTGGT
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PELICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 2067
LENGTH: 1740
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; LOCATION: (1)..(1740)
US-10-156-761-2067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI
APPLICANT: IXEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
APPLICANT: SAKAKI, YOSHIYU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2067, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 1006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SHEA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                       189
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                                                                                                                                                                                                                                                                                    392 TGGTTTGGTGGGTGACAGCCTTAATCCGATCGTGGATGCTGTCCGCC---AATCAGATAT 448
                                                                                                                                                                                                                                                                                                                                                                                332 ACACAGCTACGCAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGAATTTA 391
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TCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATAT
                                          GATCACCGGCAAGCTCGCCGCCTGCGCCGGCTCCTGCGGCCCCCGGGAACCTCCACCTCAT 248
                                                                                          CGACTGGATCCACGTCCGGCACGAGGGGGACCGCCCTTCGCCGCGGGGCGCGGAGGCGCA
                                                                                                                                                                                            TGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAATCGTT
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HORIKAWA, HIROSHI
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57.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 522.6; DB 14;
Pred. No. 4.5e-161;
0; Mismatches 719;
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TAAGTTGAGCTCGGTGGTAGAGACGTACACATAACGTCGAGAAGCATGTGCCTATTCA 1405
                CATGCTGCTGGAGCTTCTGACCGTTAAGCTGCACCAACTTCCGCTGAAGGCTGTGGT
                                                                                                                                                                                                                                                            GACACCGGGATGTGCAATGTCTGGGCGGCCCGCTACATCTCG---CCCAACGGACGCCG
                                                                               CGCCCAGTTCACCGACCGGAACCGGCAGGTCGTCTCGATGTCCGGCGACGGTGGATTCGC
                                                                                                                                                                                                  CGACTITGTGGGTTCATTCCGCCACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGG
                                                                                                                           TGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCGCGATGTGTGGCGATGGTGGTTTGGG 1645
                                                                                                                                                                        CCGCGTCATCGCCTCGTTCTCGCACGGCTCCATGGCGAACGCGCTGCCGATGGCGATCGG
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                                                                                               ; NAME/KEY: CDS
; LOCATION: (1).
US-09-815-242-9898
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/791,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR BAPPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
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       Query Match 16.0%;
Best Local Similarity 52.5%;
Matches 904; Conservative
                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 9898
LENGTH: 1719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9898, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 10110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                 TYPE: DNA
ORGANISM: Salmonella
                                                                                                                                                                   FEATURE:
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Zyskind, Judith W.
Wall, Daniel
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Yamamoto, Robert T.
Xu, H. Howard
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    Score 344.8; DB 9;
Pred. No. 2.1e-102;
0; Mismatches 797;
                                              Length 1719;
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                                 GAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACATAACGTCGAGAAGCATGTGCCT
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  TATCGGGACGCCCGTAAAGGGCTTGATGACTTAGCCAAACTCAGCGATAA-
                                                                                                                  TTGCCTCATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGATCGGATGCTCAAGGCACAC
                                                                                                                                                                                              CGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCTGCAACAATCGAAAATATT 1280
                                                                                                                                                                                                                                      GCCTTTTATCCGAGCGATGCCAAAATCATTCAGATTGACATCAACCCGGGCAGTATTGGC
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                                                                            CTGCCGCTGGTGGAAGAAAAAGCAATCGTAAATTCCTCGATAAAGCTCT---GGAACAC
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; TYPE: DNA ; ORGANISM: Corynebacterium glutamicum 

)WS-09-965-825-12
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; Sequence 12, Application US/09965825

; Patent No. US20020150999A1
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                                                                                                                           SOFTWARE: Patentin
SEQ ID NO 12
                                                                                                                                                    APPLICANT: THICKES, HERMANN
APPLICANT: THICKES, HERMANN
APPLICANT: THICKES, HERMANN
APPLICANT: THICKES, GEORGES
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC F
TITLE OF INVENTION: CORYNEFORM BACTERIA
TITLE REFERENCE: 21354USOX
CURRENT APPLICATION NUMBER: US/09/965,825
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: DE 10048604.5
PRIOR APPLICATION NUMBER: DE 10117085.8
PRIOR APPLICATION NUMBER: DE 10117085.8
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                    Query Match
                                                                                                            LENGTH: 1422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCATCGATGGCCCGGTACTGGTTGACGTGGTCGTGGCAAAAGAAGAAGCTGGCGATCCCG
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                                                                                                                                              version 3.1
 15.0%;
Score 324.4; DB
Pred. No. 1e-95;
                 DB 10;
               Length 1422;
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Дb	Qy	Qy Db	Qy Db	Qy Db	Qy Db
301 698	241 638	181 578	121 518	61 458	1 398
AATAGCCATAACGTTGAGGAGTTCAG 326	AAGCGTGGCAACAACTGGAATTTAAGAGCACAATTGAAGTCGCACCAAGTTAGGCAACAC 300	GGGCATCCCTGTTTGGTACCGAGTACCCACCCGGGCCTGAAACTCCCTGGCAGGCGGGCC 240	TIGGITICGACGGGCTGAAACCAAACCAGACTGCCCAGCAACGACGGAAATCCCCAAAAGT 180	. CGAGGCGACCAGACAGGCGTGCCCACGATGTTTAAATAGGCGATCGGTGGGCATCTGTGT 120 	TTAGAGGCGATTCTGTGAGGTCACTTTTTGTGGGGTCGGGGTCTAAATTTGGCCAGTTTT 60

Search completed: October 3, 2003, 21:08:46 Job time : $568 \ \text{secs}$